

OM protein - protein search, using sw model

Run on: April 8, 2004, 15:30:06 ; Search time 43.3077 Seconds  
(without alignments)  
71.766 Million cell updates/sec

Title: US-09-787-443A-19  
Perfect score: 11  
Sequence: 1 AEGGKKKKMRA 11

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 1586107 seqs, 282547505 residues

Word size : 0

Total number of hits satisfying chosen parameters: 22883

Minimum DB seq length: 11  
Maximum DB seq length: 11

Post-processing: Listing first 100 summaries

Database : A\_Geneseq\_29Jan04:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Query		Match	Length	DB	ID	Description
	Score	%					
1	11	100.0	11	3	AAy88547	Aay88547 NCAM Ig1	
2	11	100.0	11	5	ABG69347	Abg69347 Human neu	
3	6	54.5	11	2	AAR60841	Aar60841 Polyoxime	
4	5	45.5	11	4	ABP14556	Abp14556 HIV A03 s	
5	5	45.5	11	4	ABP14558	Abp14558 HIV A03 s	
6	5	45.5	11	4	ABP22767	Abp22767 HIV A11 m	
7	5	45.5	11	4	ABP17206	Abp17206 HIV B27 s	
8	5	45.5	11	4	ABP14557	Abp14557 HIV A03 s	
9	5	45.5	11	4	ABP20732	Abp20732 HIV A03 m	

10	5	45.5	11	4	ABP20406	Abp20406	HIV A03 m
11	5	45.5	11	4	ABP20558	Abp20558	HIV A03 m
12	5	45.5	11	4	ABP22878	Abp22878	HIV A11 m
13	5	45.5	11	4	ABP17204	Abp17204	HIV B27 s
14	5	45.5	11	4	ABP17205	Abp17205	HIV B27 s
15	5	45.5	11	5	ABB74598	Abb74598	Transcrip
16	5	45.5	11	5	ABB74599	Abb74599	Transcrip
17	5	45.5	11	6	ABU69054	Abu69054	Intercell
18	5	45.5	11	6	ABU69005	Abu69005	Intercell
19	5	45.5	11	6	ABU69004	Abu69004	Intercell
20	5	45.5	11	6	ABU69056	Abu69056	Intercell
21	4	36.4	11	2	AAR30180	Aar30180	PPI-2:T32
22	4	36.4	11	2	AAR55163	Aar55163	Fragment
23	4	36.4	11	2	AAR72301	Aar72301	Anti-HIV
24	4	36.4	11	2	AAR85318	Aar85318	Human ret
25	4	36.4	11	2	AAW24438	Aaw24438	Nucleic a
26	4	36.4	11	2	AAW38865	Aaw38865	Delivery
27	4	36.4	11	2	AAW38785	Aaw38785	Delivery
28	4	36.4	11	2	AAW38822	Aaw38822	Delivery
29	4	36.4	11	2	AAW26074	Aaw26074	M32 deriv
30	4	36.4	11	2	AAW16616	Aaw16616	Phosphoin
31	4	36.4	11	2	AAW86735	Aaw86735	Anticoagu
32	4	36.4	11	2	AAW77457	Aaw77457	Lipophili
33	4	36.4	11	3	AAy88559	Aay88559	NCAM Igl
34	4	36.4	11	3	AAy88558	Aay88558	NCAM Igl
35	4	36.4	11	3	AAy79943	Aay79943	Beta-amyl
36	4	36.4	11	3	AAy90160	Aay90160	UPAR targ
37	4	36.4	11	3	AAy95530	Aay95530	Transacti
38	4	36.4	11	3	AAB29168	Aab29168	Peptide #
39	4	36.4	11	4	AAB50076	Aab50076	csk tyros
40	4	36.4	11	4	AAM42176	Aam42176	Human pol
41	4	36.4	11	4	AAB31770	Aab31770	Amino aci
42	4	36.4	11	4	ABP19373	Abp19373	HIV B62 s
43	4	36.4	11	4	ABP13804	Abp13804	HIV A02 s
44	4	36.4	11	4	ABP17176	Abp17176	HIV B27 s
45	4	36.4	11	4	ABP13805	Abp13805	HIV A02 s
46	4	36.4	11	5	AAU76079	Aau76079	Nocicepti
47	4	36.4	11	5	AAU76110	Aau76110	Nocicepti
48	4	36.4	11	5	AAU96727	Aau96727	Molecular
49	4	36.4	11	5	ABB74600	Abb74600	Transcrip
50	4	36.4	11	5	ABB74327	Abb74327	Bipartite
51	4	36.4	11	5	ABG67641	Abg67641	Human ADP
52	4	36.4	11	5	ABG70612	Abg70612	[Lys]11 1
53	4	36.4	11	6	ABP98787	Abp98787	Peptide #
54	4	36.4	11	6	AAO27080	Aao27080	Fibrinoge
55	4	36.4	11	6	AAO27103	Aao27103	Fibrinoge
56	4	36.4	11	6	ADA18540	Ada18540	Human alp
57	4	36.4	11	6	ADA26448	Ada26448	Suitable
58	4	36.4	11	6	ADA23765	Ada23765	Alzheimer
59	4	36.4	11	7	ADC35041	Adc35041	RhoA prot
60	4	36.4	11	7	ADC35004	Adc35004	Rho-like
61	4	36.4	11	7	ADE10861	Adel0861	Chimeric
62	3	27.3	11	2	AAR24537	Aar24537	Sequence
63	3	27.3	11	2	AAR24543	Aar24543	Sequence
64	3	27.3	11	2	AAR24539	Aar24539	Sequence
65	3	27.3	11	2	AAR24536	Aar24536	Sequence
66	3	27.3	11	2	AAR27765	Aar27765	BSA-bindi

67	3	27.3	11	2	AAR27771	Aar27771	BSA-bindi
68	3	27.3	11	2	AAR41837	Aar41837	Phospholi
69	3	27.3	11	2	AAR41846	Aar41846	Phospholi
70	3	27.3	11	2	AAR41844	Aar41844	Phospholi
71	3	27.3	11	2	AAR41830	Aar41830	Phospholi
72	3	27.3	11	2	AAR41843	Aar41843	Phospholi
73	3	27.3	11	2	AAR41842	Aar41842	Phospholi
74	3	27.3	11	2	AAR41853	Aar41853	Phospholi
75	3	27.3	11	2	AAR41845	Aar41845	Phospholi
76	3	27.3	11	2	AAR41838	Aar41838	Phospholi
77	3	27.3	11	2	AAR41840	Aar41840	Phospholi
78	3	27.3	11	2	AAR41847	Aar41847	Phospholi
79	3	27.3	11	2	AAR41841	Aar41841	Phospholi
80	3	27.3	11	2	AAR41849	Aar41849	Phospholi
81	3	27.3	11	2	AAR41850	Aar41850	Phospholi
82	3	27.3	11	2	AAR41851	Aar41851	Phospholi
83	3	27.3	11	2	AAR41836	Aar41836	Phospholi
84	3	27.3	11	2	AAR41852	Aar41852	Phospholi
85	3	27.3	11	2	AAR41839	Aar41839	Phospholi
86	3	27.3	11	2	AAR41848	Aar41848	Phospholi
87	3	27.3	11	2	AAR36639	Aar36639	Group I s
88	3	27.3	11	2	AAR43429	Aar43429	Ro/SSA ep
89	3	27.3	11	2	AAR31493	Aar31493	P3 OF 31-
90	3	27.3	11	2	AAR61919	Aar61919	PLP pepti
91	3	27.3	11	2	AAR61920	Aar61920	PLP pepti
92	3	27.3	11	2	AAR60400	Aar60400	Antiproli
93	3	27.3	11	2	AAR60401	Aar60401	Antiproli
94	3	27.3	11	2	AAR70274	Aar70274	Thrombosp
95	3	27.3	11	2	AAR70297	Aar70297	Subpeptid
96	3	27.3	11	2	AAR72299	Aar72299	Anti-HIV
97	3	27.3	11	2	AAR79718	Aar79718	Optimal p
98	3	27.3	11	2	AAR90267	Aar90267	Ion-chann
99	3	27.3	11	2	AAR71901	Aar71901	Cladospor
100	3	27.3	11	2	AAR66819	Aar66819	Mouse syn

#### ALIGNMENTS

##### RESULT 1

AAAY88547

ID AAY88547 standard; peptide; 11 AA.

XX

AC AAY88547;

XX

DT 07-AUG-2000 (first entry)

XX

DE NCAM Igl binding peptide #19.

XX

KW NCAM; neural cell adhesion molecule; Igl; immunoglobulin domain 1;

KW neurite outgrowth promoter; proliferation; nerve damage; sclerosis;

KW impaired myelination; stroke; Parkinson's disease; memory; schizophrenia;

KW Alzheimer's disease; diabetes mellitus; circadian clock; nephrosis;

KW treatment; prosthetic nerve guide; treatment; nervous system.

XX

OS Synthetic.

XX

PN WO200018801-A2.  
 XX  
 PD 06-APR-2000.  
 XX  
 PF 23-SEP-1999; 99WO-DK000500.  
 XX  
 PR 29-SEP-1998; 98DK-00001232.  
 PR 29-APR-1999; 99DK-00000592.  
 XX  
 PA (RONN/) RONN L C B.  
 PA (BOCK/) BOCK E.  
 PA (HOLM/) HOLM A.  
 PA (OLSE/) OLSEN M.  
 PA (OSTE/) OSTERGAARD S.  
 PA (JENS/) JENSEN P H.  
 PA (POUL/) POULSEN F M.  
 PA (SORO/) SOROKA V.  
 PA (RALE/) RALETS I.  
 PA (BERE/) BEREZIN V.  
 XX  
 PI Ronn LCB, Bock E, Holm A, Olsen M, Ostergaard S, Jensen PH;  
 PI Poulsen FM, Soroka V, Ralets I, Berezin V;  
 XX  
 DR WPI; 2000-293111/25.  
 XX  
 PT Compositions that bind neural cell adhesion molecules useful for treating  
 PT disorders of the nervous system and muscles e.g. Alzheimer's and  
 PT Parkinson's diseases.  
 XX  
 PS Example 4; Page 25; 119pp; English.  
 XX  
 CC Neural cell adhesion molecule (NCAM) is a cellular adhesion molecule.  
 CC NCAM is found in three forms, two of which are transmembrane forms, while  
 CC the third is attached via a lipid anchor to the cell membrane. All three  
 CC NCAM forms have an extracellular structure consisting five immunoglobulin  
 CC domains (Ig domains). The Ig domains are numbered 1 to 5 from the N-  
 CC terminal. The present sequence represents a peptide which binds to the  
 CC NCAM Ig1 domain. The peptide can be used in a compound which binds to  
 CC NCAM-Ig1/Ig2 domains, and is capable of stimulating or promoting neurite  
 CC outgrowth from NCAM presenting cells, and is also capable of promoting  
 CC the proliferation of NCAM presenting cells. The compound may be used in  
 CC the treatment of normal, degenerated or damaged NCAM presenting cells.  
 CC The compound may in particular be used to treat diseases of the central  
 CC and peripheral nervous systems such as post operative nerve damage,  
 CC traumatic nerve damage, impaired myelination of nerve fibres, conditions  
 CC resulting from a stroke, Parkinson's disease, Alzheimer's disease,  
 CC dementias, sclerosis, nerve degeneration associated with diabetes  
 CC mellitus, disorders affecting the circadian clock or neuro-muscular  
 CC transmission and schizophrenia. Conditions affecting the muscles may also  
 CC be treated with the compound, such as conditions associated with impaired  
 CC function of neuromuscular connections (e.g. genetic or traumatic shock or  
 CC traumatic atrophic muscle disorders). Conditions of the gonads, pancreas  
 CC (e.g. diabetes mellitus types I and II), kidney (e.g. nephrosis), heart,  
 CC liver and bowel may also be treated using the compound. The compound is  
 CC used in a prosthetic nerve guide, and also to stimulate the ability to  
 CC learn, and to stimulate the memory of a subject  
 XX



SQ Sequence 11 AA;

Query Match 100.0%; Score 11; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.0001;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEGGKKKKMRA 11  
| | | | | | | | | |  
Db 1 AEGGKKKKMRA 11

RESULT 2

ABG69347

ID ABG69347 standard; peptide; 11 AA.

XX

AC ABG69347;

XX

DT 21-OCT-2002 (first entry)

XX

DE Human neural cell adhesion molecule (NCAM) peptide #19.

XX

KW Human; neural cell adhesion molecule; NCAM; heart muscle cell survival;

KW acute myocardial infarction; central nervous system disorder; stroke;

KW peripheral nervous system disorder; postoperative nerve damage;

KW traumatic nerve damage; spinal cord injury; nerve fibre; schizophrenia;

KW postischaemic damage; multiinfarct dementia; multiple sclerosis;

KW nerve degeneration; diabetes mellitus; neuro-muscular degeneration;

KW Alzheimer's disease; Parkinson's disease;

KW Huntington's disease. atrophic muscle disorder; gonad degeneration;

KW nephrosis.

XX

OS Homo sapiens.

XX

PN WO200247719-A2.

XX

PD 20-JUN-2002.

XX

PF 12-DEC-2001; 2001WO-DK000822.

XX

PR 12-DEC-2000; 2000DK-00001863.

XX

PA (ENKA-) ENKAM PHARM AS.

XX

PI Bock E, Berezin V, Kohler LB;

XX

DR WPI; 2002-583473/62.

XX

PT Use of a compound comprising a peptide of neural cell adhesion molecule,

PT in the preparation of medicament for preventing death of cells presenting

PT NCAM or NCAM ligand and treating central nervous system diseases.

XX

PS Disclosure; Page 16; 57pp; English.

XX

CC The invention relates to use of a compound (I) comprising a peptide which

CC comprises at least 5 contiguous amino acid residues of a sequence of the

CC neural cell adhesion molecule (NCAM), its fragment, variant or its mimic,

CC for the preparation of a medicament for preventing death of cells

CC presenting the NCAM or an NCAM ligand. (I) is useful in the preparation  
 CC of a medicament for preventing death of cells presenting the NCAM or an  
 CC NCAM ligand. The medicament is for the stimulation of the survival of  
 CC heart muscle cells, such as survival after acute myocardial infarction.  
 CC The medicament is for the treatment of diseases or conditions of the  
 CC central and peripheral nervous system, such as postoperative nerve  
 CC damage, traumatic nerve damage, e.g. resulting from spinal cord injury,  
 CC impaired myelination of nerve fibres, postischaemic damage, e.g.  
 CC resulting from a stroke, multiinfarct dementia, multiple sclerosis, nerve  
 CC degeneration associated with diabetes mellitus, neuro-muscular  
 CC degeneration, schizophrenia, Alzheimer's disease, Parkinson's disease and  
 CC Huntington's disease. The medicament is for the treatment of diseases or  
 CC conditions of the muscles including conditions with impaired function of  
 CC neuro-muscular connections, such as genetic or traumatic atrophic muscle  
 CC disorders, and for the treatment of diseases or conditions of various  
 CC organs, such as degenerative conditions of the gonads, pancreas (e.g.  
 CC diabetes mellitus type I and II) and kidney (e.g. nephrosis). ABG69329-  
 CC ABG69352 represent human NCAM peptides of the invention  
 XX  
 SQ Sequence 11 AA;

Query Match 100.0%; Score 11; DB 5; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 0.0001;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEGGKKKKMRA 11  
 |||||  
 Db 1 AEGGKKKKMRA 11

# RESULT 3

AAR60841

ID AAR60841 standard; peptide; 11 AA.

XX

AC AAR60841;

XX

DT 25-MAR-2003 (revised)

DT 05-JUN-1995 (first entry)

XX

DE Polyoxime octa-GXL baseplate.

XX

KW Polyoxime; homopolyoxime; heteropolyoxime; peptide presentation;

KW cell imaging; complementary orthogonal specifically active molecule;

KW COSM; baseplate; immunogen.

XX

OS Synthetic.

XX

FH	Key	Location/Qualifiers
FT	Modified-site	1
FT		/label= OTHER
FT		/note= "glyoxyl-glycine"
FT	Modified-site	4
FT		/label= OTHER
FT		/note= "glyoxyl-lysine"
FT	Modified-site	5
FT		/label= OTHER
FT		/note= "glyoxyl-lysine"

FT Modified-site 6  
 FT /label= OTHER  
 FT /note= "glyoxyl-lysine"  
 FT Modified-site 7  
 FT /label= OTHER  
 FT /note= "glyoxyl-lysine"  
 FT Modified-site 8  
 FT /label= OTHER  
 FT /note= "glyoxyl-lysine"  
 FT Modified-site 9  
 FT /label= OTHER  
 FT /note= "glyoxyl-lysine"  
 FT Modified-site 10  
 FT /label= OTHER  
 FT /note= "glyoxyl-lysine"  
 XX  
 PN WO9425071-A1.  
 XX  
 PD 10-NOV-1994.  
 XX  
 PF 05-MAY-1994; 94WO-IB0000093.  
 XX  
 PR 05-MAY-1993; 93US-00057594.  
 PR 31-AUG-1993; 93US-00105904.  
 PR 31-AUG-1993; 93US-00114877.  
 XX  
 PA (ROSE/) ROSE K.  
 PA (OFFO/) OFFORD R E.  
 XX  
 PI Rose K, Offord RE;  
 XX  
 DR WPI; 1994-357918/44.  
 XX  
 PT Homo- and hetero-polyoxime compounds and their preparation - used for  
 PT peptide presentation to antibodies and in cell imaging etc.  
 XX  
 PS Disclosure; Page 53; 85pp; English.  
 XX  
 CC Peptides given in AAR60833-62 are used as baseplates and COSMs for the  
 CC preparation of polyoximes having varying spacing, charge, lipophilicity,  
 CC valency, conformational restraints, solubility and other physical and  
 CC biological properties. An octa-GXL baseplate structure is given in  
 CC AAR60841. (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 11 AA;

Query Match 54.5%; Score 6; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 12;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GGK KKK 8  
 |||||  
 Db 2 GGK KKK 7

RESULT 4  
 ABP14556

ID ABP14556 standard; peptide; 11 AA.  
XX  
AC ABP14556;  
XX  
DT 11-SEP-2003 (revised)  
DT 15-JUL-2002 (first entry)  
XX  
DE HIV A03 super motif gag peptide #118.  
XX  
KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;  
KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;  
KW vaccine; HIV infection; immunisation; virucide.  
XX  
OS Human immunodeficiency virus 1.  
XX  
PN WO200124810-A1.  
XX  
PD 12-APR-2001.  
XX  
PF 05-OCT-2000; 2000WO-US027766.  
XX  
PR 05-OCT-1999; 99US-00412863.  
XX  
PA (EPIM-) EPIMMUNE INC.  
XX  
PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;  
PI Baker DM, Celis E, Kubo RT, Grey HM;  
XX  
DR WPI; 2001-354887/37.  
XX  
PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)  
PT peptide groups, useful for vaccinating against HIV-1.  
XX  
PS Claim 32; Page 166; 448pp; English.  
XX  
CC The present invention describes a composition (I) comprising a prepared  
CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
CC sequence selected from 51 defined amino acid sequences (ABL25347 to  
CC ABP25397). (I) has virucide activity and can be used in vaccines. (I) may  
CC be used for immunising subjects against HIV-1 infections. The use of  
CC group-based vaccines has several advantages over traditional vaccines,  
CC particularly when compared to the use of whole antigens in vaccine  
CC compositions. There is evidence that the immune response to whole  
CC antigens is directed largely toward variable regions of the antigen,  
CC allowing for immune escape due to mutations. The groups for inclusion in  
CC an group-based vaccine may be selected from conserved regions of viral or  
CC tumour-associated antigens, which therefore reduces the likelihood of  
CC escape mutants. Furthermore, immunosuppressive groups that may be present  
CC in whole antigens can be avoided with the use of group-based vaccines. An  
CC additional advantage of an group-based vaccine approach is the ability to  
CC combine selected groups (CTL and HTL), and further, to modify the  
CC composition of the groups, achieving, for example, enhanced  
CC immunogenicity. Accordingly, the immune response can be modulated, as  
CC appropriate, for the target disease. Similar engineering of the response  
CC is not possible with traditional approaches. ABP11501 to ABP25412  
CC represent peptide sequences used in the exemplification of the present  
CC invention. (Updated on 11-SEP-2003 to standardise OS field)

XX

SQ Sequence 11 AA;

Query Match 45.5%; Score 5; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GGKKK 7  
|||||  
Db 7 GGKKK 11

RESULT 5

ABP14558

ID ABP14558 standard; peptide; 11 AA.

XX

AC ABP14558;

XX

DT 11-SEP-2003 (revised)

DT 15-JUL-2002 (first entry)

XX

DE HIV A03 super motif gag peptide #120.

XX

KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;  
KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;  
KW vaccine; HIV infection; immunisation; virucide.

XX

OS Human immunodeficiency virus 1.

XX

PN WO200124810-A1.

XX

PD 12-APR-2001.

XX

PF 05-OCT-2000; 2000WO-US027766.

XX

PR 05-OCT-1999; 99US-00412863.

XX

PA (EPIM-) EPIMMUNE INC.

XX

PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;

PI Baker DM, Celis E, Kubo RT, Grey HM;

XX

DR WPI; 2001-354887/37.

XX

PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)  
PT peptide groups, useful for vaccinating against HIV-1.

XX

PS Claim 32; Page 166; 448pp; English.

XX

CC The present invention describes a composition (I) comprising a prepared  
CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
CC sequence selected from 51 defined amino acid sequences (ABL25347 to  
CC ABP25397). (I) has virucide activity and can be used in vaccines. (I) may  
CC be used for immunising subjects against HIV-1 infections. The use of  
CC group-based vaccines has several advantages over traditional vaccines,  
CC particularly when compared to the use of whole antigens in vaccine  
CC compositions. There is evidence that the immune response to whole

CC antigens is directed largely toward variable regions of the antigen,  
CC allowing for immune escape due to mutations. The groups for inclusion in  
CC an group-based vaccine may be selected from conserved regions of viral or  
CC tumour-associated antigens, which therefore reduces the likelihood of  
CC escape mutants. Furthermore, immunosuppressive groups that may be present  
CC in whole antigens can be avoided with the use of group-based vaccines. An  
CC additional advantage of an group-based vaccine approach is the ability to  
CC combine selected groups (CTL and HTL), and further, to modify the  
CC composition of the groups, achieving, for example, enhanced  
CC immunogenicity. Accordingly, the immune response can be modulated, as  
CC appropriate, for the target disease. Similar engineering of the response  
CC is not possible with traditional approaches. ABP11501 to ABP25412  
CC represent peptide sequences used in the exemplification of the present  
CC invention. (Updated on 11-SEP-2003 to standardise OS field)

XX

SQ Sequence 11 AA;

Query Match 45.5%; Score 5; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GGKKK 7

|||||

Db 5 GGKKK 9

#### RESULT 6

ABP22767

ID ABP22767 standard; peptide; 11 AA.

XX

AC ABP22767;

XX

DT 11-SEP-2003 (revised)

DT 15-JUL-2002 (first entry)

XX

DE HIV All motif gag peptide #146.

XX

KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;

KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;

KW vaccine; HIV infection; immunisation; virucide.

XX

OS Human immunodeficiency virus 1.

XX

PN WO200124810-A1.

XX

PD 12-APR-2001.

XX

PF 05-OCT-2000; 2000WO-US027766.

XX

PR 05-OCT-1999; 99US-00412863.

XX

PA (EPIM-) EPIMMUNE INC.

XX

PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;

PI Baker DM, Celis E, Kubo RT, Grey HM;

XX

DR WPI; 2001-354887/37.

XX  
PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)  
PT peptide groups, useful for vaccinating against HIV-1.  
XX  
PS Claim 32; Page 335; 448pp; English.  
XX  
CC The present invention describes a composition (I) comprising a prepared  
CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
CC sequence selected from 51 defined amino acid sequences (ABL25347 to  
CC ABP25397). (I) has virucide activity and can be used in vaccines. (I) may  
CC be used for immunising subjects against HIV-1 infections. The use of  
CC group-based vaccines has several advantages over traditional vaccines,  
CC particularly when compared to the use of whole antigens in vaccine  
CC compositions. There is evidence that the immune response to whole  
CC antigens is directed largely toward variable regions of the antigen,  
CC allowing for immune escape due to mutations. The groups for inclusion in  
CC an group-based vaccine may be selected from conserved regions of viral or  
CC tumour-associated antigens, which therefore reduces the likelihood of  
CC escape mutants. Furthermore, immunosuppressive groups that may be present  
CC in whole antigens can be avoided with the use of group-based vaccines. An  
CC additional advantage of an group-based vaccine approach is the ability to  
CC combine selected groups (CTL and HTL), and further, to modify the  
CC composition of the groups, achieving, for example, enhanced  
CC immunogenicity. Accordingly, the immune response can be modulated, as  
CC appropriate, for the target disease. Similar engineering of the response  
CC is not possible with traditional approaches. ABP11501 to ABP25412  
CC represent peptide sequences used in the exemplification of the present  
CC invention. (Updated on 11-SEP-2003 to standardise OS field)  
XX  
SQ Sequence 11 AA;

Query Match 45.5%; Score 5; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GGKKK 7  
| | | | |  
Db 1 GGKKK 5

RESULT 7  
ABP17206  
ID ABP17206 standard; peptide; 11 AA.  
XX  
AC ABP17206;  
XX  
DT 11-SEP-2003 (revised)  
DT 15-JUL-2002 (first entry)  
XX  
DE HIV B27 super motif gag peptide #82.  
XX  
KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;  
KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;  
KW vaccine; HIV infection; immunisation; virucide.  
XX  
OS Human immunodeficiency virus 1.  
XX

PN WO200124810-A1.  
 XX  
 PD 12-APR-2001.  
 XX  
 PF 05-OCT-2000; 2000WO-US027766.  
 XX  
 PR 05-OCT-1999; 99US-00412863.  
 XX  
 PA (EPIM-) EPIMMUNE INC.  
 XX  
 PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;  
 PI Baker DM, Celis E, Kubo RT, Grey HM;  
 XX  
 DR WPI; 2001-354887/37.  
 XX  
 PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)  
 PT peptide groups, useful for vaccinating against HIV-1.  
 XX  
 PS Claim 32; Page 221; 448pp; English.  
 XX  
 CC The present invention describes a composition (I) comprising a prepared  
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
 CC sequence selected from 51 defined amino acid sequences (ABL25347 to  
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I) may  
 CC be used for immunising subjects against HIV-1 infections. The use of  
 CC group-based vaccines has several advantages over traditional vaccines,  
 CC particularly when compared to the use of whole antigens in vaccine  
 CC compositions. There is evidence that the immune response to whole  
 CC antigens is directed largely toward variable regions of the antigen,  
 CC allowing for immune escape due to mutations. The groups for inclusion in  
 CC an group-based vaccine may be selected from conserved regions of viral or  
 CC tumour-associated antigens, which therefore reduces the likelihood of  
 CC escape mutants. Furthermore, immunosuppressive groups that may be present  
 CC in whole antigens can be avoided with the use of group-based vaccines. An  
 CC additional advantage of an group-based vaccine approach is the ability to  
 CC combine selected groups (CTL and HTL), and further, to modify the  
 CC composition of the groups, achieving, for example, enhanced  
 CC immunogenicity. Accordingly, the immune response can be modulated, as  
 CC appropriate, for the target disease. Similar engineering of the response  
 CC is not possible with traditional approaches. ABP11501 to ABP25412  
 CC represent peptide sequences used in the exemplification of the present  
 CC invention. (Updated on 11-SEP-2003 to standardise OS field)  
 XX  
 SQ Sequence 11 AA;

Query Match 45.5%; Score 5; DB 4; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGKKK 7  
 |||||  
 Db 4 GGKKK 8

RESULT 8  
 ABP14557  
 ID ABP14557 standard; peptide; 11 AA.



XX  
AC ABP14557;  
XX  
DT 11-SEP-2003 (revised)  
DT 15-JUL-2002 (first entry)  
XX  
DE HIV A03 super motif gag peptide #119.  
XX  
KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;  
KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;  
KW vaccine; HIV infection; immunisation; virucide.  
XX  
OS Human immunodeficiency virus 1.  
XX  
PN WO200124810-A1.  
XX  
PD 12-APR-2001.  
XX  
PF 05-OCT-2000; 2000WO-US027766.  
XX  
PR 05-OCT-1999; 99US-00412863.  
XX  
PA (EPIM-) EPIMMUNE INC.  
XX  
PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;  
PI Baker DM, Celis E, Kubo RT, Grey HM;  
XX  
DR WPI; 2001-354887/37.  
XX  
PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)  
PT peptide groups, useful for vaccinating against HIV-1.  
XX  
PS Claim 32; Page 166; 448pp; English.  
XX  
CC The present invention describes a composition (I) comprising a prepared  
CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
CC sequence selected from 51 defined amino acid sequences (ABL25347 to  
CC ABP25397). (I) has virucide activity and can be used in vaccines. (I) may  
CC be used for immunising subjects against HIV-1 infections. The use of  
CC group-based vaccines has several advantages over traditional vaccines,  
CC particularly when compared to the use of whole antigens in vaccine  
CC compositions. There is evidence that the immune response to whole  
CC antigens is directed largely toward variable regions of the antigen,  
CC allowing for immune escape due to mutations. The groups for inclusion in  
CC an group-based vaccine may be selected from conserved regions of viral or  
CC tumour-associated antigens, which therefore reduces the likelihood of  
CC escape mutants. Furthermore, immunosuppressive groups that may be present  
CC in whole antigens can be avoided with the use of group-based vaccines. An  
CC additional advantage of an group-based vaccine approach is the ability to  
CC combine selected groups (CTL and HTL), and further, to modify the  
CC composition of the groups, achieving, for example, enhanced  
CC immunogenicity. Accordingly, the immune response can be modulated, as  
CC appropriate, for the target disease. Similar engineering of the response  
CC is not possible with traditional approaches. ABP11501 to ABP25412  
CC represent peptide sequences used in the exemplification of the present  
CC invention. (Updated on 11-SEP-2003 to standardise OS field)  
XX

SQ Sequence 11 AA;

Query Match 45.5%; Score 5; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GGKKK 7  
|||||  
Db 5 GGKKK 9

RESULT 9

ABP20732

ID ABP20732 standard; peptide; 11 AA.

XX

AC ABP20732;

XX

DT 11-SEP-2003 (revised)

DT 15-JUL-2002 (first entry)

XX

DE HIV A03 motif gag peptide #395.

XX

KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;  
KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;  
KW vaccine; HIV infection; immunisation; virucide.

XX

OS Human immunodeficiency virus 1.

XX

PN WO200124810-A1.

XX

PD 12-APR-2001.

XX

PF 05-OCT-2000; 2000WO-US027766.

XX

PR 05-OCT-1999; 99US-00412863.

XX

PA (EPIM-) EPIMMUNE INC.

XX

PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;  
PI Baker DM, Celis E, Kubo RT, Grey HM;

XX

DR WPI; 2001-354887/37.

XX

PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)  
PT peptide groups, useful for vaccinating against HIV-1.

XX

PS Claim 32; Page 294; 448pp; English.

XX

CC The present invention describes a composition (I) comprising a prepared  
CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
CC sequence selected from 51 defined amino acid sequences (ABL25347 to  
CC ABP25397). (I) has virucide activity and can be used in vaccines. (I) may  
CC be used for immunising subjects against HIV-1 infections. The use of  
CC group-based vaccines has several advantages over traditional vaccines,  
CC particularly when compared to the use of whole antigens in vaccine  
CC compositions. There is evidence that the immune response to whole  
CC antigens is directed largely toward variable regions of the antigen,

CC allowing for immune escape due to mutations. The groups for inclusion in  
CC an group-based vaccine may be selected from conserved regions of viral or  
CC tumour-associated antigens, which therefore reduces the likelihood of  
CC escape mutants. Furthermore, immunosuppressive groups that may be present  
CC in whole antigens can be avoided with the use of group-based vaccines. An  
CC additional advantage of an group-based vaccine approach is the ability to  
CC combine selected groups (CTL and HTL), and further, to modify the  
CC composition of the groups, achieving, for example, enhanced  
CC immunogenicity. Accordingly, the immune response can be modulated, as  
CC appropriate, for the target disease. Similar engineering of the response  
CC is not possible with traditional approaches. ABP11501 to ABP25412  
CC represent peptide sequences used in the exemplification of the present  
CC invention. (Updated on 11-SEP-2003 to standardise OS field)

XX

SQ Sequence 11 AA;

Query Match 45.5%; Score 5; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GGKKK 7  
| | | | |  
Db 7 GGKKK 11

RESULT 10

ABP20406

ID ABP20406 standard; peptide; 11 AA.

XX

AC ABP20406;

XX

DT 11-SEP-2003 (revised)

DT 15-JUL-2002 (first entry)

XX

DE HIV A03 motif gag peptide #69.

XX

KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;  
KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;  
KW vaccine; HIV infection; immunisation; virucide.

XX

OS Human immunodeficiency virus 1.

XX

PN WO200124810-A1.

XX

PD 12-APR-2001.

XX

PF 05-OCT-2000; 2000WO-US027766.

XX

PR 05-OCT-1999; 99US-00412863.

XX

PA (EPIM-) EPIMMUNE INC.

XX

PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;

PI Baker DM, Celis E, Kubo RT, Grey HM;

XX

DR WPI; 2001-354887/37.

XX

PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)  
PT peptide groups, useful for vaccinating against HIV-1.  
XX  
PS Claim 32; Page 288; 448pp; English.  
XX  
CC The present invention describes a composition (I) comprising a prepared  
CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
CC sequence selected from 51 defined amino acid sequences (ABL25347 to  
CC ABP25397). (I) has virucide activity and can be used in vaccines. (I) may  
CC be used for immunising subjects against HIV-1 infections. The use of  
CC group-based vaccines has several advantages over traditional vaccines,  
CC particularly when compared to the use of whole antigens in vaccine  
CC compositions. There is evidence that the immune response to whole  
CC antigens is directed largely toward variable regions of the antigen,  
CC allowing for immune escape due to mutations. The groups for inclusion in  
CC an group-based vaccine may be selected from conserved regions of viral or  
CC tumour-associated antigens, which therefore reduces the likelihood of  
CC escape mutants. Furthermore, immunosuppressive groups that may be present  
CC in whole antigens can be avoided with the use of group-based vaccines. An  
CC additional advantage of an group-based vaccine approach is the ability to  
CC combine selected groups (CTL and HTL), and further, to modify the  
CC composition of the groups, achieving, for example, enhanced  
CC immunogenicity. Accordingly, the immune response can be modulated, as  
CC appropriate, for the target disease. Similar engineering of the response  
CC is not possible with traditional approaches. ABP11501 to ABP25412  
CC represent peptide sequences used in the exemplification of the present  
CC invention. (Updated on 11-SEP-2003 to standardise OS field)  
XX  
SQ Sequence 11 AA;

Query Match 45.5%; Score 5; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GGKKK 7  
| | | | |  
Db 1 GGKKK 5

RESULT 11  
ABP20558  
ID ABP20558 standard; peptide; 11 AA.  
XX  
AC ABP20558;  
XX  
DT 11-SEP-2003 (revised)  
DT 15-JUL-2002 (first entry)  
XX  
DE HIV A03 motif gag peptide #221.  
XX  
KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;  
KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;  
KW vaccine; HIV infection; immunisation; virucide.  
XX  
OS Human immunodeficiency virus 1.  
XX  
PN WO200124810-A1.

XX  
 PD 12-APR-2001.  
 XX  
 PF 05-OCT-2000; 2000WO-US027766.  
 XX  
 PR 05-OCT-1999; 99US-00412863.  
 XX  
 PA (EPIM-) EPIMMUNE INC.  
 XX  
 PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;  
 PI Baker DM, Celis E, Kubo RT, Grey HM;  
 XX  
 DR WPI; 2001-354887/37.  
 XX  
 PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)  
 PT peptide groups, useful for vaccinating against HIV-1.  
 XX  
 PS Claim 32; Page 291; 448pp; English.  
 XX  
 CC The present invention describes a composition (I) comprising a prepared  
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
 CC sequence selected from 51 defined amino acid sequences (ABL25347 to  
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I) may  
 CC be used for immunising subjects against HIV-1 infections. The use of  
 CC group-based vaccines has several advantages over traditional vaccines;  
 CC particularly when compared to the use of whole antigens in vaccine  
 CC compositions. There is evidence that the immune response to whole  
 CC antigens is directed largely toward variable regions of the antigen,  
 CC allowing for immune escape due to mutations. The groups for inclusion in  
 CC an group-based vaccine may be selected from conserved regions of viral or  
 CC tumour-associated antigens, which therefore reduces the likelihood of  
 CC escape mutants. Furthermore, immunosuppressive groups that may be present  
 CC in whole antigens can be avoided with the use of group-based vaccines. An  
 CC additional advantage of an group-based vaccine approach is the ability to  
 CC combine selected groups (CTL and HTL), and further, to modify the  
 CC composition of the groups, achieving, for example, enhanced  
 CC immunogenicity. Accordingly, the immune response can be modulated, as  
 CC appropriate, for the target disease. Similar engineering of the response  
 CC is not possible with traditional approaches. ABP11501 to ABP25412  
 CC represent peptide sequences used in the exemplification of the present  
 CC invention. (Updated on 11-SEP-2003 to standardise OS field)  
 XX  
 SQ Sequence 11 AA;

Query Match 45.5%; Score 5; DB 4; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GGKKK 7  
 |||||  
 Db 1 GGKKK 5

RESULT 12  
 ABP22878  
 ID ABP22878 standard; peptide; 11 AA.  
 XX

AC ABP22878;  
XX  
DT 11-SEP-2003 (revised)  
DT 15-JUL-2002 (first entry)  
XX  
DE HIV All motif gag peptide #257.  
XX  
KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;  
KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;  
KW vaccine; HIV infection; immunisation; virucide.  
XX  
OS Human immunodeficiency virus 1.  
XX  
PN WO200124810-A1.  
XX  
PD 12-APR-2001.  
XX  
PF 05-OCT-2000; 2000WO-US027766.  
XX  
PR 05-OCT-1999; 99US-00412863.  
XX  
PA (EPIM-) EPIMMUNE INC.  
XX  
PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;  
PI Baker DM, Celis E, Kubo RT, Grey HM;  
XX  
DR WPI; 2001-354887/37.  
XX  
PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)  
PT peptide groups, useful for vaccinating against HIV-1.  
XX  
PS Claim 32; Page 338; 448pp; English.  
XX  
CC The present invention describes a composition (I) comprising a prepared  
CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
CC sequence selected from 51 defined amino acid sequences (ABL25347 to  
CC ABP25397). (I) has virucide activity and can be used in vaccines. (I) may  
CC be used for immunising subjects against HIV-1 infections. The use of  
CC group-based vaccines has several advantages over traditional vaccines,  
CC particularly when compared to the use of whole antigens in vaccine  
CC compositions. There is evidence that the immune response to whole  
CC antigens is directed largely toward variable regions of the antigen,  
CC allowing for immune escape due to mutations. The groups for inclusion in  
CC an group-based vaccine may be selected from conserved regions of viral or  
CC tumour-associated antigens, which therefore reduces the likelihood of  
CC escape mutants. Furthermore, immunosuppressive groups that may be present  
CC in whole antigens can be avoided with the use of group-based vaccines. An  
CC additional advantage of an group-based vaccine approach is the ability to  
CC combine selected groups (CTL and HTL), and further, to modify the  
CC composition of the groups, achieving, for example, enhanced  
CC immunogenicity. Accordingly, the immune response can be modulated, as  
CC appropriate, for the target disease. Similar engineering of the response  
CC is not possible with traditional approaches. ABP11501 to ABP25412  
CC represent peptide sequences used in the exemplification of the present  
CC invention. (Updated on 11-SEP-2003 to standardise OS field)  
XX  
SQ Sequence 11 AA;

Query Match 45.5%; Score 5; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GGKKK 7  
|||||  
Db 7 GGKKK 11

RESULT 13

ABP17204

ID ABP17204 standard; peptide; 11 AA.

XX

AC ABP17204;

XX

DT 11-SEP-2003 (revised)

DT 15-JUL-2002 (first entry)

XX

DE HIV B27 super motif gag peptide #80.

XX

KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;

KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;

KW vaccine; HIV infection; immunisation; virucide.

XX

OS Human immunodeficiency virus 1.

XX

PN WO200124810-A1.

XX

PD 12-APR-2001.

XX

PF 05-OCT-2000; 2000WO-US027766.

XX

PR 05-OCT-1999; 99US-00412863.

XX

PA (EPIM-) EPIMMUNE INC.

XX

PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;

PI Baker DM, Celis E, Kubo RT, Grey HM;

XX

DR WPI; 2001-354887/37.

XX

PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)

PT peptide groups, useful for vaccinating against HIV-1.

XX

PS Claim 32; Page 221; 448pp; English.

XX

CC The present invention describes a composition (I) comprising a prepared

CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid

CC sequence selected from 51 defined amino acid sequences (ABL25347 to

CC ABP25397). (I) has virucide activity and can be used in vaccines. (I) may

CC be used for immunising subjects against HIV-1 infections. The use of

CC group-based vaccines has several advantages over traditional vaccines,

CC particularly when compared to the use of whole antigens in vaccine

CC compositions. There is evidence that the immune response to whole

CC antigens is directed largely toward variable regions of the antigen,

CC allowing for immune escape due to mutations. The groups for inclusion in

CC an group-based vaccine may be selected from conserved regions of viral or  
CC tumour-associated antigens, which therefore reduces the likelihood of  
CC escape mutants. Furthermore, immunosuppressive groups that may be present  
CC in whole antigens can be avoided with the use of group-based vaccines. An  
CC additional advantage of an group-based vaccine approach is the ability to  
CC combine selected groups (CTL and HTL), and further, to modify the  
CC composition of the groups, achieving, for example, enhanced  
CC immunogenicity. Accordingly, the immune response can be modulated, as  
CC appropriate, for the target disease. Similar engineering of the response  
CC is not possible with traditional approaches. ABP11501 to ABP25412  
CC represent peptide sequences used in the exemplification of the present  
CC invention. (Updated on 11-SEP-2003 to standardise OS field)

XX

SQ Sequence 11 AA;

Query Match 45.5%; Score 5; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GGKKK 7  
| | | | |  
Db 6 GGKKK 10

#### RESULT 14

ABP17205

ID ABP17205 standard; peptide; 11 AA.

XX

AC ABP17205;

XX

DT 11-SEP-2003 (revised)

DT 15-JUL-2002 (first entry)

XX

DE HIV B27 super motif gag peptide #81.

XX

KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;

KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;

KW vaccine; HIV infection; immunisation; virucide.

XX

OS Human immunodeficiency virus 1.

XX

PN WO200124810-A1.

XX

PD 12-APR-2001.

XX

PF 05-OCT-2000; 2000WO-US027766.

XX

PR 05-OCT-1999; 99US-00412863.

XX

PA (EPIM-) EPIMMUNE INC.

XX

PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;

PI Baker DM, Celis E, Kubo RT, Grey HM;

XX

DR WPI; 2001-354887/37.

XX

PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)



PT peptide groups, useful for vaccinating against HIV-1.

XX

PS Claim 32; Page 221; 448pp; English.

XX

CC The present invention describes a composition (I) comprising a prepared  
CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
CC sequence selected from 51 defined amino acid sequences (ABL25347 to  
CC ABP25397). (I) has virucide activity and can be used in vaccines. (I) may  
CC be used for immunising subjects against HIV-1 infections. The use of  
CC group-based vaccines has several advantages over traditional vaccines,  
CC particularly when compared to the use of whole antigens in vaccine  
CC compositions. There is evidence that the immune response to whole  
CC antigens is directed largely toward variable regions of the antigen,  
CC allowing for immune escape due to mutations. The groups for inclusion in  
CC an group-based vaccine may be selected from conserved regions of viral or  
CC tumour-associated antigens, which therefore reduces the likelihood of  
CC escape mutants. Furthermore, immunosuppressive groups that may be present  
CC in whole antigens can be avoided with the use of group-based vaccines. An  
CC additional advantage of an group-based vaccine approach is the ability to  
CC combine selected groups (CTL and HTL), and further, to modify the  
CC composition of the groups, achieving, for example, enhanced  
CC immunogenicity. Accordingly, the immune response can be modulated, as  
CC appropriate, for the target disease. Similar engineering of the response  
CC is not possible with traditional approaches. ABP11501 to ABP25412  
CC represent peptide sequences used in the exemplification of the present  
CC invention. (Updated on 11-SEP-2003 to standardise OS field)

XX

SQ Sequence 11 AA;

Query Match 45.5%; Score 5; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GGKKK 7

|||||

Db 4 GGKKK 8

RESULT 15

ABB74598

ID ABB74598 standard; peptide; 11 AA.

XX

AC ABB74598;

XX

DT 18-APR-2002 (first entry)

XX

DE Transcription factor nuclear localisation signal peptide SEQ ID NO:362.

XX

KW Fusogenic; nuclear localisation signal; NLS; encapsulation; lipogene;

KW liposome; micelle; karyophilic; cytostatic; antitumour; solid tumour;

KW peptide-lipid-polynucleotide complex; neoplastic disease; gene therapy;

KW breast carcinoma; prostate carcinoma.

XX

OS Mus sp.

XX

PN WO200193836-A2.

XX

PD 13-DEC-2001.  
 XX  
 PF 08-JUN-2001; 2001WO-US018657.  
 XX  
 PR 09-JUN-2000; 2000US-0210925P.  
 XX  
 PA (BOUL/) BOULIKAS T.  
 XX  
 PI Boulikas T;  
 XX  
 DR WPI; 2002-164295/21.  
 XX  
 PT Encapsulation of plasmid DNA (Lipogenes) and therapeutic agents with  
 PT nuclear localization signal/fusogenic peptide conjugates into targeted  
 PT liposome complexes.  
 XX  
 PS Claim 14; Page 76; 107pp; English.  
 XX  
 CC The present invention describes a method for producing micelles with  
 CC entrapped therapeutic agents. The method comprises: (1) combining  
 CC negatively charged agent with a cationic lipid in a ratio where 30-90 %  
 CC of the negatively charged atoms are neutralised by positive charges on  
 CC lipid molecules to form an electrostatic micelle complex in 20-80 %  
 CC ethanol; and (2) combining the micelle complex of (a) with fusogenic-  
 CC karyophilic peptide conjugates in a 0.0-0.3 ratio, therefore producing  
 CC micelles with entrapped therapeutic agents. Also described is a method  
 CC for delivering a therapeutic agent in vivo, comprising the administration  
 CC of the micelle. ABB74256 to ABB74858 represent specifically claimed  
 CC nuclear localisation signal (NLS) peptides for use in the method as the  
 CC fusogenic-karyophilic peptides. The micelles produced can have cytostatic  
 CC and antitumour activities. The peptide-lipid-polynucleotide complexes  
 CC produced are useful for inhibiting the progression of neoplastic  
 CC diseases. The invention relates to the field of gene therapy and is  
 CC directed toward methods for producing peptide-lipid-polynucleotide  
 CC complexes suitable for delivery of polynucleotides. The encapsulated  
 CC molecules display therapeutic efficacy in eradicating solid tumours  
 CC including but not limited to breast carcinoma or prostate carcinoma.  
 CC ABB74235 to ABB74255 are used in the exemplification of the present  
 CC invention  
 XX  
 SQ Sequence 11 AA;

Query Match 45.5%; Score 5; DB 5; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GK KKK 8  
 |||||  
 Db 1 GK KKK 5

RESULT 16  
 ABB74599  
 ID ABB74599 standard; peptide; 11 AA.  
 XX  
 AC ABB74599;  
 XX

DT 18-APR-2002 (first entry)  
 XX  
 DE Transcription factor nuclear localisation signal peptide SEQ ID NO:363.  
 XX  
 KW Fusogenic; nuclear localisation signal; NLS; encapsulation; lipogene;  
 KW liposome; micelle; karyophilic; cytostatic; antitumour; solid tumour;  
 KW peptide-lipid-polynucleotide complex; neoplastic disease; gene therapy;  
 KW breast carcinoma; prostate carcinoma.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200193836-A2.  
 XX  
 PD 13-DEC-2001.  
 XX  
 PF 08-JUN-2001; 2001WO-US018657.  
 XX  
 PR 09-JUN-2000; 2000US-0210925P.  
 XX  
 PA (BOUL/) BOULIKAS T.  
 XX  
 PI Boulikas T;  
 XX  
 DR WPI; 2002-164295/21.  
 XX  
 PT Encapsulation of plasmid DNA (Lipogenes) and therapeutic agents with  
 PT nuclear localization signal/fusogenic peptide conjugates into targeted  
 PT liposome complexes.  
 XX  
 PS Claim 14; Page 76; 107pp; English.  
 XX  
 CC The present invention describes a method for producing micelles with  
 CC entrapped therapeutic agents. The method comprises: (1) combining  
 CC negatively charged agent with a cationic lipid in a ratio where 30-90 %  
 CC of the negatively charged atoms are neutralised by positive charges on  
 CC lipid molecules to form an electrostatic micelle complex in 20-80 %  
 CC ethanol; and (2) combining the micelle complex of (a) with fusogenic-  
 CC karyophilic peptide conjugates in a 0.0-0.3 ratio, therefore producing  
 CC micelles with entrapped therapeutic agents. Also described is a method  
 CC for delivering a therapeutic agent in vivo, comprising the administration  
 CC of the micelle. ABB74256 to ABB74858 represent specifically claimed  
 CC nuclear localisation signal (NLS) peptides for use in the method as the  
 CC fusogenic-karyophilic peptides. The micelles produced can have cytostatic  
 CC and antitumour activities. The peptide-lipid-polynucleotide complexes  
 CC produced are useful for inhibiting the progression of neoplastic  
 CC diseases. The invention relates to the field of gene therapy and is  
 CC directed toward methods for producing peptide-lipid-polynucleotide  
 CC complexes suitable for delivery of polynucleotides. The encapsulated  
 CC molecules display therapeutic efficacy in eradicating solid tumours  
 CC including but not limited to breast carcinoma or prostate carcinoma.  
 CC ABB74235 to ABB74255 are used in the exemplification of the present  
 CC invention  
 XX  
 SQ Sequence 11 AA;

Query Match 45.5%; Score 5; DB 5; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GKKKK 8  
|||||  
Db 1 GKKKK 5

RESULT 17

ABU69054

ID ABU69054 standard; peptide; 11 AA.

XX

AC ABU69054;

XX

DT 24-JUN-2003 (first entry)

XX

DE Intercellular communication antiarrhythmic peptide #1312.

XX

KW Antiarrhythmic peptide; non-proliferative disease;

KW intercellular communication; CaCl<sub>2</sub> arrhythmia mouse model; arrhythmia;

KW gap junctional intracellular communication; GIJC; gap junction;

KW metabolic stress; antithrombosis; ulcer; infertility; osteoporosis;

KW joint disease; arthritis; vascularisation; cornea; cataract; deafness;

KW gastrointestinal motility disorder; heart contractility; psychosis;

KW depression; glucose tolerance; non-insulin dependent diabetes mellitus;

KW cancer; pancreatitis; inflammation; incontinence; diabetic retinopathy;

KW diabetic neuropathy; neuropathic pain; spinal cord injury;

KW dental tissue disorder; kidney disease; ischaemia;

KW neurodegenerative disease; Parkinson's disease; reactive gliosis;

KW glial neoplasm; hormone secretion; tobacco.

XX

OS Synthetic.

XX

PN WO200277017-A2.

XX

PD 03-OCT-2002.

XX

PF 22-FEB-2002; 2002WO-US005773.

XX

PR 22-FEB-2001; 2001US-00792286.

PR 22-FEB-2001; 2001WO-DK000127.

PR 23-AUG-2001; 2001US-0314470P.

XX

PA (ZEAL-) ZEALAND PHARM AS.

XX

PI Larsen BD, Petersen JS, Meier E, Kjolbye AL, Jorgensen NR;

PI Nielsen MS, Holstein-Rathlou N, Martins JB;

XX

DR WPI; 2003-229193/22.

XX

PT A pharmaceutical composition useful for the treatment of e.g. arrhythmia

PT comprises an antiarrhythmic peptides and a carrier.

XX

PS Example 51 (synthesis); Page 188; 233pp; English.

XX

CC The invention discloses a pharmaceutical composition which comprises

CC antiarrhythmic peptide(s) and a carrier with an improved stability. The

CC peptides can be used for the prevention or treatment of a non-

CC proliferative disease involving administering a compound that facilitates  
 CC intercellular communication as determined by effect in the CaCl<sub>2</sub>  
 CC arrhythmia mouse model. They can also be used for the treatment of  
 CC arrhythmia, diseases associated with impaired gap junctional  
 CC intracellular communication (GIJC) during metabolic stress,  
 CC antithrombosis, wound and lesions in skin or oral mucosa, ulcers,  
 CC infertility, for prevention and/or treatment of slowed conduction in the  
 CC heart, osteoporosis, joint diseases e.g. arthritis, vascularisation of  
 CC the cornea, cataract, deafness associated with impaired GIJC,  
 CC gastrointestinal motility disorders, for improving heart contractility,  
 CC for treating organic psychoses e.g. depression, improving glucose  
 CC tolerance in non-insulin dependent diabetes mellitus patients, for  
 CC treating or preventing spreading of cancer, pancreatitis, glucose and  
 CC oxygen deprivation of cells, tissue or organs (e.g. heart), treating  
 CC inflammation of airway epithelium, disorders of alveolar tissue, urinary  
 CC bladder incontinence, impaired hearing, diabetic retinopathy, diabetic  
 CC neuropathy, neuropathic pain, spinal cord injuries, dental tissue  
 CC disorders, kidney diseases, failures of bone marrow or stem cell  
 CC transplantation, for treating ischaemia, neurodegenerative disease (e.g.  
 CC Parkinson's disease), reactive gliosis, vascular abnormalities in the  
 CC retina, inflammation, treating or preventing the development of glial  
 CC neoplasms, for improving the vascular healing process after balloon  
 CC catheter injury in the carotid, for treating reduced capacity of  
 CC haematopoietic tissue, treating inappropriate hormone secretion from the  
 CC anterior pituitary gland, prevention or treatment of disturbed  
 CC development of teeth, for amelioration of skin aging and cellulite and  
 CC for the treatment of tobacco related disease associated with uncoupling  
 CC of gap junctions. The sequences presented in ABU67743-ABU69079 are the  
 CC modified peptides disclosed in the invention

XX

SQ Sequence 11 AA;

Query Match 45.5%; Score 5; DB 6; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GK KKK 8

|||||

Db 5 GK KKK 9

RESULT 18

ABU69005

ID ABU69005 standard; peptide; 11 AA.

XX

AC ABU69005;

XX

DT 24-JUN-2003 (first entry)

XX

DE Intercellular communication antiarrhythmic peptide #1263.

XX

KW Antiarrhythmic peptide; non-proliferative disease;

KW intercellular communication; CaCl<sub>2</sub> arrhythmia mouse model; arrhythmia;

KW gap junctional intracellular communication; GIJC; gap junction;

KW metabolic stress; antithrombosis; ulcer; infertility; osteoporosis;

KW joint disease; arthritis; vascularisation; cornea; cataract; deafness;

KW gastrointestinal motility disorder; heart contractility; psychosis;

KW depression; glucose tolerance; non-insulin dependent diabetes mellitus;  
 KW cancer; pancreatitis; inflammation; incontinence; diabetic retinopathy;  
 KW diabetic neuropathy; neuropathic pain; spinal cord injury;  
 KW dental tissue disorder; kidney disease; ischaemia;  
 KW neurodegenerative disease; Parkinson's disease; reactive gliosis;  
 KW glial neoplasm; hormone secretion; tobacco.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200277017-A2.  
 XX  
 PD 03-OCT-2002.  
 XX  
 PF 22-FEB-2002; 2002WO-US005773.  
 XX  
 PR 22-FEB-2001; 2001US-00792286.  
 PR 22-FEB-2001; 2001WO-DK000127.  
 PR 23-AUG-2001; 2001US-0314470P.  
 XX  
 PA (ZEAL-) ZEALAND PHARM AS.  
 XX  
 PI Larsen BD, Petersen JS, Meier E, Kjolbye AL, Jorgensen NR;  
 PI Nielsen MS, Holstein-Rathlou N, Martins JB;  
 XX  
 DR WPI; 2003-229193/22.  
 XX  
 PT A pharmaceutical composition useful for the treatment of e.g. arrhythmia  
 PT comprises an antiarrhythmic peptides and a carrier.  
 XX  
 PS Example 9 (experimental); Page 146; 233pp; English.  
 XX  
 CC The invention discloses a pharmaceutical composition which comprises  
 CC antiarrhythmic peptide(s) and a carrier with an improved stability. The  
 CC peptides can be used for the prevention or treatment of a non-  
 CC proliferative disease involving administering a compound that facilitates  
 CC intercellular communication as determined by effect in the CaCl<sub>2</sub>  
 CC arrhythmia mouse model. They can also be used for the treatment of  
 CC arrhythmia, diseases associated with impaired gap junctional  
 CC intracellular communication (GIJC) during metabolic stress,  
 CC antithrombosis, wound and lesions in skin or oral mucosa, ulcers,  
 CC infertility, for prevention and/or treatment of slowed conduction in the  
 CC heart, osteoporosis, joint diseases e.g. arthritis, vascularisation of  
 CC the cornea, cataract, deafness associated with impaired GJIC,  
 CC gastrointestinal motility disorders, for improving heart contractility,  
 CC for treating organic psychoses e.g. depression, improving glucose  
 CC tolerance in non-insulin dependent diabetes mellitus patients, for  
 CC treating or preventing spreading of cancer, pancreatitis, glucose and  
 CC oxygen deprivation of cells, tissue or organs (e.g. heart), treating  
 CC inflammation of airway epithelium, disorders of alveolar tissue, urinary  
 CC bladder incontinence, impaired hearing, diabetic retinopathy, diabetic  
 CC neuropathy, neuropathic pain, spinal cord injuries, dental tissue  
 CC disorders, kidney diseases, failures of bone marrow or stem cell  
 CC transplantation, for treating ischaemia, neurodegenerative disease (e.g.  
 CC Parkinson's disease), reactive gliosis, vascular abnormalities in the  
 CC retina, inflammation, treating or preventing the development of glial  
 CC neoplasms, for improving the vascular healing process after balloon  
 CC catheter injury in the carotid, for treating reduced capacity of

CC haematopoietic tissue, treating inappropriate hormone secretion from the  
CC anterior pituitary gland, prevention or treatment of disturbed  
CC development of teeth, for amelioration of skin aging and cellulite and  
CC for the treatment of tobacco related disease associated with uncoupling  
CC of gap junctions. The sequences presented in ABU67743-ABU69079 are the  
CC modified peptides disclosed in the invention

XX

SQ Sequence 11 AA;

Query Match 45.5%; Score 5; DB 6; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GKKKK 8

||||

Db 5 GKKKK 9

RESULT 19

ABU69004

ID ABU69004 standard; peptide; 11 AA.

XX

AC ABU69004;

XX

DT 24-JUN-2003 (first entry)

XX

DE Intercellular communication antiarrhythmic peptide #1262.

XX

KW Antiarrhythmic peptide; non-proliferative disease;

KW intercellular communication; CaCl<sub>2</sub> arrhythmia mouse model; arrhythmia;

KW gap junctional intracellular communication; GIJC; gap junction;

KW metabolic stress; antithrombosis; ulcer; infertility; osteoporosis;

KW joint disease; arthritis; vascularisation; cornea; cataract; deafness;

KW gastrointestinal motility disorder; heart contractility; psychosis;

KW depression; glucose tolerance; non-insulin dependent diabetes mellitus;

KW cancer; pancreatitis; inflammation; incontinence; diabetic retinopathy;

KW diabetic neuropathy; neuropathic pain; spinal cord injury;

KW dental tissue disorder; kidney disease; ischaemia;

KW neurodegenerative disease; Parkinson's disease; reactive gliosis;

KW glial neoplasm; hormone secretion; tobacco.

XX

OS Synthetic.

XX

PN WO200277017-A2.

XX

PD 03-OCT-2002.

XX

PF 22-FEB-2002; 2002WO-US005773.

XX

PR 22-FEB-2001; 2001US-00792286.

PR 22-FEB-2001; 2001WO-DK000127.

PR 23-AUG-2001; 2001US-0314470P.

XX

PA (ZEAL-) ZEALAND PHARM AS.

XX

PI Larsen BD, Petersen JS, Meier E, Kjolbye AL, Jorgensen NR;

PI Nielsen MS, Holstein-Rathlou N, Martins JB;

XX  
DR WPI; 2003-229193/22.  
XX  
PT A pharmaceutical composition useful for the treatment of e.g. arrhythmia  
PT comprises an antiarrhythmic peptides and a carrier.  
XX  
PS Example 9 (experimental); Page 146; 233pp; English.  
XX  
CC The invention discloses a pharmaceutical composition which comprises  
CC antiarrhythmic peptide(s) and a carrier with an improved stability. The  
CC peptides can be used for the prevention or treatment of a non-  
CC proliferative disease involving administering a compound that facilitates  
CC intercellular communication as determined by effect in the CaCl<sub>2</sub>  
CC arrhythmia mouse model. They can also be used for the treatment of  
CC arrhythmia, diseases associated with impaired gap junctional  
CC intracellular communication (GIJC) during metabolic stress,  
CC antithrombosis, wound and lesions in skin or oral mucosa, ulcers,  
CC infertility, for prevention and/or treatment of slowed conduction in the  
CC heart, osteoporosis, joint diseases e.g. arthritis, vascularisation of  
CC the cornea, cataract, deafness associated with impaired GJIC,  
CC gastrointestinal motility disorders, for improving heart contractility,  
CC for treating organic psychoses e.g. depression, improving glucose  
CC tolerance in non-insulin dependent diabetes mellitus patients, for  
CC treating or preventing spreading of cancer, pancreatitis, glucose and  
CC oxygen deprivation of cells, tissue or organs (e.g. heart), treating  
CC inflammation of airway epithelium, disorders of alveolar tissue, urinary  
CC bladder incontinence, impaired hearing, diabetic retinopathy, diabetic  
CC neuropathy, neuropathic pain, spinal cord injuries, dental tissue  
CC disorders, kidney diseases, failures of bone marrow or stem cell  
CC transplantation, for treating ischaemia, neurodegenerative disease (e.g.  
CC Parkinson's disease), reactive gliosis, vascular abnormalities in the  
CC retina, inflammation, treating or preventing the development of glial  
CC neoplasms, for improving the vascular healing process after balloon  
CC catheter injury in the carotid, for treating reduced capacity of  
CC haematopoietic tissue, treating inappropriate hormone secretion from the  
CC anterior pituitary gland, prevention or treatment of disturbed  
CC development of teeth, for amelioration of skin aging and cellulite and  
CC for the treatment of tobacco related disease associated with uncoupling  
CC of gap junctions. The sequences presented in ABU67743-ABU69079 are the  
CC modified peptides disclosed in the invention  
XX  
SQ Sequence 11 AA;

Query Match 45.5%; Score 5; DB 6; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GK KKK 8  
| | | | |  
Db 5 GK KKK 9

RESULT 20  
ABU69056  
ID ABU69056 standard; peptide; 11 AA.  
XX  
AC ABU69056;



XX  
 DT 24-JUN-2003 (first entry)  
 XX  
 DE Intercellular communication antiarrhythmic peptide #1314.  
 XX  
 KW Antiarrhythmic peptide; non-proliferative disease;  
 KW intercellular communication; CaCl<sub>2</sub> arrhythmia mouse model; arrhythmia;  
 KW gap junctional intracellular communication; GIJC; gap junction;  
 KW metabolic stress; antithrombosis; ulcer; infertility; osteoporosis;  
 KW joint disease; arthritis; vascularisation; cornea; cataract; deafness;  
 KW gastrointestinal motility disorder; heart contractility; psychosis;  
 KW depression; glucose tolerance; non-insulin dependent diabetes mellitus;  
 KW cancer; pancreatitis; inflammation; incontinence; diabetic retinopathy;  
 KW diabetic neuropathy; neuropathic pain; spinal cord injury;  
 KW dental tissue disorder; kidney disease; ischaemia;  
 KW neurodegenerative disease; Parkinson's disease; reactive gliosis;  
 KW glial neoplasm; hormone secretion; tobacco.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200277017-A2.  
 XX  
 PD 03-OCT-2002.  
 XX  
 PF 22-FEB-2002; 2002WO-US005773.  
 XX  
 PR 22-FEB-2001; 2001US-00792286.  
 PR 22-FEB-2001; 2001WO-DK000127.  
 PR 23-AUG-2001; 2001US-0314470P.  
 XX  
 PA (ZEAL-) ZEALAND PHARM AS.  
 XX  
 PI Larsen BD, Petersen JS, Meier E, Kjolbye AL, Jorgensen NR;  
 PI Nielsen MS, Holstein-Rathlou N, Martins JB;  
 XX  
 DR WPI; 2003-229193/22.  
 XX  
 PT A pharmaceutical composition useful for the treatment of e.g. arrhythmia  
 PT comprises an antiarrhythmic peptides and a carrier.  
 XX  
 PS Example 52 (synthesis); Page 189; 233pp; English.  
 XX  
 CC The invention discloses a pharmaceutical composition which comprises  
 CC antiarrhythmic peptide(s) and a carrier with an improved stability. The  
 CC peptides can be used for the prevention or treatment of a non-  
 CC proliferative disease involving administering a compound that facilitates  
 CC intercellular communication as determined by effect in the CaCl<sub>2</sub>  
 CC arrhythmia mouse model. They can also be used for the treatment of  
 CC arrhythmia, diseases associated with impaired gap junctional  
 CC intracellular communication (GIJC) during metabolic stress,  
 CC antithrombosis, wound and lesions in skin or oral mucosa, ulcers,  
 CC infertility, for prevention and/or treatment of slowed conduction in the  
 CC heart, osteoporosis, joint diseases e.g. arthritis, vascularisation of  
 CC the cornea, cataract, deafness associated with impaired GIJC,  
 CC gastrointestinal motility disorders, for improving heart contractility,  
 CC for treating organic psychoses e.g. depression, improving glucose  
 CC tolerance in non-insulin dependent diabetes mellitus patients, for

CC treating or preventing spreading of cancer, pancreatitis, glucose and  
 CC oxygen deprivation of cells, tissue or organs (e.g. heart), treating  
 CC inflammation of airway epithelium, disorders of alveolar tissue, urinary  
 CC bladder incontinence, impaired hearing, diabetic retinopathy, diabetic  
 CC neuropathy, neuropathic pain, spinal cord injuries, dental tissue  
 CC disorders, kidney diseases, failures of bone marrow or stem cell  
 CC transplantation, for treating ischaemia, neurodegenerative disease (e.g.  
 CC Parkinson's disease), reactive gliosis, vascular abnormalities in the  
 CC retina, inflammation, treating or preventing the development of glial  
 CC neoplasms, for improving the vascular healing process after balloon  
 CC catheter injury in the carotid, for treating reduced capacity of  
 CC haematopoietic tissue, treating inappropriate hormone secretion from the  
 CC anterior pituitary gland, prevention or treatment of disturbed  
 CC development of teeth, for amelioration of skin aging and cellulite and  
 CC for the treatment of tobacco related disease associated with uncoupling  
 CC of gap junctions. The sequences presented in ABU67743-ABU69079 are the  
 CC modified peptides disclosed in the invention

XX

SQ Sequence 11 AA;

Query Match 45.5%; Score 5; DB 6; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GK KKK 8  
 |||||  
 Db 5 GK KKK 9

RESULT 21

AAR30180

ID AAR30180 standard; protein; 11 AA.

XX

AC AAR30180;

XX

DT 25-MAR-2003 (revised)

DT 05-MAY-1993 (first entry)

XX

DE PPI-2:T32 N-terminal sequence.

XX

KW Potato papain inhibitor; cystatin; plant; agriculture; transgenic;  
 KW potato; cysteine protease inhibitor.

XX

OS Solanum tuberosum.

XX

PN W09221753-A1.

XX

PD 10-DEC-1992.

XX

PF 08-JUN-1992; 92WO-US004785.

XX

PR 07-JUN-1991; 91US-00712024.

XX

PA (DOWC ) DOWELANCO.

XX

PI Walsh TA, Owens Merlo PA, Strickland JA, Orr GL, Merlo DJ;

PI Waldron C;

XX  
 DR WPI; 1992-433651/52.  
 XX  
 PT Mid-gut effective plant nystatin and DNA encoding it - used for  
 PT protecting a plant against insects having digestive cysteine protease(s).  
 XX  
 PS Disclosure; Fig 3; 96pp; English.  
 XX  
 CC The sequence shows the N-terminal sequence of a peptide fragment of  
 CC potato papain inhibitor (PPI) obtained by digestion with trypsin. A  
 CC number of fragments were N-terminal sequenced, and extensive homology was  
 CC found, indicating related fragments. These data indicate that PPI  
 CC consists of 8 domains that are all closely related and are members of the  
 CC cystatin family of cysteine protease inhibitors. See also AAR30177-86.  
 CC (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EGGK 5  
 ||||  
 Db 8 EGGK 11

# RESULT 22

AAR55163

ID AAR55163 standard; protein; 11 AA.

XX

AC AAR55163;

XX

DT 25-MAR-2003 (revised)

DT 11-JAN-1995 (first entry)

XX

DE Fragment of retinoic acid receptor RAR-beta.

XX

KW Liver; hap; retinoic acid receptor; steroid; thyroid; hormone; hepatoma;  
 KW retinoid; antibody.

XX

OS Homo sapiens.

XX

PN US5317090-A.

XX

PD 31-MAY-1994.

XX

PF 11-DEC-1992; 92US-00989902.

XX

PR 16-DEC-1987; 87US-00133687.

PR 17-DEC-1987; 87US-00134130.

PR 20-JUN-1988; 88US-00209009.

PR 30-NOV-1988; 88US-00278136.

PR 30-MAR-1989; 89US-00330405.

PR 21-AUG-1991; 91US-00751612.

PR 30-MAR-1992; 92US-00860577.

XX

PA (INSP ) INST PASTEUR.  
 XX  
 PI Marchio A, Chambon P, Petkovich M, Krust A, Dejean A, Tiollais P;  
 PI Brand N, De The HB;  
 XX  
 DR WPI; 1994-176333/21.  
 XX  
 PT Antibody specific for retinoic acid receptor-beta - useful for detecting,  
 PT quantifying and identifying agonists and antagonists of retinoid  
 PT activity.  
 XX  
 PS Claim 4; Col 40; 35pp; English.  
 XX  
 CC The retinoic acid receptor RAR-beta is encoded by a gene designated hap.  
 CC The hap gene is transcribed at low level in most human tissues, but the  
 CC gene is overexpressed in prostate and kidney. Six out of seven hepatoma or  
 CC hepatoma-derived cell lines express a small hap transcript which is  
 CC undetectable in normal adult and foetal livers but present in all non-  
 CC hepatic tissues tested. (Updated on 25-MAR-2003 to correct PF field.)  
 XX  
 SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KKKK 8  
 ||||  
 Db 5 KKKK 8

# RESULT 23

AAR72301

ID AAR72301 standard; peptide; 11 AA.

XX

AC AAR72301;

XX

DT 25-MAR-2003 (revised)

DT 20-OCT-1995 (first entry)

XX

DE Anti-HIV MBPC.3.

XX

KW Multiple branch peptide construction; MBPC; HIV-1;

KW human immunodeficiency virus type 1; virucide.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Peptide 1. .6

FT /note= "peptide is present 168 times, each attached to 1  
 FT of 8 lysine residues (position 7), in dendritic  
 FT structure"

FT Misc-difference 7

FT /note= "lysine at position 7 is present 8 times, each  
 FT attached to 1 of 4 other lysine residues (position 8) and  
 FT also to 1 of 16 peptide moieties (position 1-6) in  
 FT dendritic structure"

FT Misc-difference 8  
 FT /note= "lysine at position 8 is present 4 times, each  
 FT attached to other lysines (positions 7 and 9) in  
 FT dendritic structure"  
 FT Misc-difference 9  
 FT /note= "lysine at position 9 is present 2 times, each  
 FT attached to 1 of 4 other lysine residues (position 8) and  
 FT to a core lysine residue (position 10), in dendritic  
 FT structure"  
 FT Modified-site 11  
 FT /label= bAla, bAla-NH2  
 XX  
 PN WO9507929-A1.  
 XX  
 PD 23-MAR-1995.  
 XX  
 PF 13-SEP-1994; 94WO-GB001992.  
 XX  
 PR 13-SEP-1993; 93GB-00018901.  
 PR 15-JUN-1994; 94US-00260086.  
 XX  
 PA (ARME-) ARMEL SA.  
 PA (MCKE/) MCKELVEY I E.  
 XX  
 PI Sabatier JM, Benjouad A, Yahi N, Fenouillet E, Mabrouk K;  
 PI Gluckman J, Van Rietschoten J, Rochat H;  
 XX  
 DR WPI; 1995-131312/17.  
 XX  
 PT Multiple branch peptide constructions formed from the V3 loop of HIV-1  
 PT gp120 - used to treat HIV infection.  
 XX  
 PS Disclosure; Page 5; 39pp; English.  
 XX  
 CC Multiple branch peptide constructions (given in AAR72299-301) are formed  
 CC from the V3 loop of HIV-1 gp120. Each MBPC includes multiple peptide  
 CC moieties incorporating the GPGR consensus sequence, each attached to the  
 CC amino group of a lysine residue, forming a dendritic structure. (Updated  
 CC on 25-MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KKKK 8  
 | | | |  
 Db 7 KKKK 10

RESULT 24  
 AAR85318  
 ID AAR85318 standard; peptide; 11 AA.  
 XX  
 AC AAR85318;  
 XX

DT 25-MAR-2003 (revised)  
 DT 19-AUG-1996 (first entry)  
 XX  
 DE Human retinoic acid receptor RAR-beta (human liver HAP) peptide-2.  
 XX  
 KW HAP; liver; hepatoma; retinoic acid receptor; RAR-beta; psoriasis;  
 KW atherosclerosis; rheumatoid arthritis.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US5468617-A.  
 XX  
 PD 21-NOV-1995.  
 XX  
 PF 02-FEB-1994; 94US-00190555.  
 XX  
 PR 16-DEC-1987; 87US-00133687.  
 PR 17-DEC-1987; 87US-00134130.  
 PR 20-JUN-1988; 88US-00209009.  
 PR 30-NOV-1988; 88US-00278136.  
 PR 30-MAR-1989; 89US-00330405.  
 PR 21-AUG-1991; 91US-00751612.  
 PR 30-MAR-1992; 92US-00860577.  
 PR 11-DEC-1992; 92US-00989902.  
 PR 22-JUL-1993; 93US-00095706.  
 XX  
 PA (TIOL/) TIOLLAIS P.  
 PA (DEJE/) DEJEAN A.  
 PA (KRUS/) KRUST A.  
 PA (PETK/) PETKOVICH M.  
 PA (DTHE/) BLAUDIN DE THE H.  
 PA (MARC/) MARCHIO A.  
 PA (BRAN/) BRAND N.  
 PA (CHAM/) CHAMBON P.  
 XX  
 PI Brand N, Chambon P, Blandin De The H, Marchio A, Dejean A;  
 PI Petkovich M, Krust A, Tiollais P;  
 XX  
 DR WPI; 1996-010094/01.  
 XX  
 PT Method for screening for retinoic acid receptor-beta (ant)agonists -  
 PT useful for blood testing and for treatment of rheumatoid arthritis,  
 PT psoriasis, atherosclerosis etc.  
 XX  
 PS Claim 7; Col 39-40; 35pp; English.  
 XX  
 CC This RAR-beta peptide-2 fragment is part of a protein which may be  
 CC expressed recombinantly in bacterial host cells such as Escherichia coli  
 CC TG-1. The protein, which is free from human, blood-derived protein, forms  
 CC a complex with an agonist or antagonist. The protein may be used in a  
 CC novel method for assaying a fluid for the presence of an agonist or  
 CC antagonist to retinoic acid receptor, RAR-beta. (Updated on 25-MAR-2003  
 CC to correct PF field.)  
 XX  
 SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KKKK 8  
||||  
Db 5 KKKK 8

RESULT 25

AAW24438

ID AAW24438 standard; peptide; 11 AA.

XX

AC AAW24438;

XX

DT 30-SEP-1997 (first entry)

XX

DE Nucleic acid (NA) binding peptide used in NA delivery to cells.

XX

KW Nucleic acid transporter; gene therapy; binding complex; lysis agent;

KW JTS-1; K8; alpha helix; endosome; lysosome; nucleus targeting.

XX

OS Synthetic.

XX

PN WO9640958-A1.

XX

PD 19-DEC-1996.

XX

PF 23-APR-1996; 96WO-US005679.

XX

PR 07-JUN-1995; 95US-00484777.

XX

PA (BAYU ) BAYLOR COLLEGE MEDICINE.

XX

PI Smith LC, Sparrow JT, Woo SL;

XX

DR WPI; 1997-052345/05.

XX

PT Nucleic acid transporter useful in gene therapy - contains binding  
PT complex associated with surface and nuclear ligands and lysis agent.

XX

PS Disclosure; Page 49; 125pp; English.

XX

CC AAW24434-W24459 are nucleic acid (NA) binding peptides, capable of both  
CC condensing and stabilising a NA. The peptides can be conjugated to a  
CC lytic peptide to form a nucleic acid transporter system. The lysis agent  
CC forms an alpha-helical structure. The transporter system is used to  
CC deliver nucleic acid to a cell and for treating humans by gene therapy.  
CC By taking advantage of the characteristics of both the lysis agents and  
CC the binding molecules, delivery of the nucleic acid is enhanced. Specific  
CC lysis agents are capable of releasing the nucleic acid into the cellular  
CC interior from the endosome. Release is efficient without  
CC endosomal/lysosomal degradation. Once released the binding complexes help  
CC target the nucleic acid to the nucleus

XX

SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KKKK 8  
||||  
Db 4 KKKK 7

RESULT 26

AAW38865

ID AAW38865 standard; peptide; 11 AA.

XX

AC AAW38865;

XX

DT 30-MAR-1998 (first entry)

XX

DE Delivery peptide used in peptide macromolecule complex.

XX

KW Delivery peptide; peptide-macromolecule complex; macromolecule delivery;

KW non-exchangeable lipophilic peptide; disease therapy; cell targeting.

XX

OS Synthetic.

XX

PN WO9725070-A2.

XX

PD 17-JUL-1997.

XX

PF 02-JAN-1997; 97WO-US000454.

XX

PR 08-JAN-1996; 96US-00584043.

XX

PA (BAYU ) BAYLOR COLLEGE MEDICINE.

XX

PI Smith LC, Sparrow JT, Hauer J, Mims MP;

XX

DR WPI; 1997-372622/34.

XX

PT New lipophilic peptide-macromolecule complexes - used for the delivery of  
PT macromolecules to cells, particularly for gene therapy.

XX

PS Disclosure; Page 51; 106pp; English.

XX

CC This sequence represents a delivery peptide that can be used in the  
CC peptide-macromolecule complex of the invention. The peptide-macromolecule  
CC complex of the invention is for delivering a macromolecule into a cell,  
CC and comprises a non-exchangeable lipophilic peptide (LP) comprising a  
CC delivery peptide associated with a lipid moiety, where the delivery  
CC peptide portion of the LP is complexed to the macromolecule. The  
CC complexes can be used for the delivery of macromolecules such as nucleic  
CC acids, proteins, oligonucleotides, lipids or carbohydrates. They can be  
CC used to treat diseases by enhancing delivery of specific nucleic acid to  
CC the appropriate targeted cells. They can also be used to create  
CC transformed cells as well as transgenic animals for assessing human  
CC disease in an animal model. They can also be used for livestock  
CC agricultural purposes. The complex is capable of transporting the  
CC macromolecule in a stable and condensed state and releasing the molecule  
CC into the cellular interior. The complex can bind with a cell surface



CC receptor, lyse an endosome and target the nucleus of the cell

XX

SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 1.2e+03;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KKKK 8

||||

Db 1 KKKK 4

# RESULT 27

AAW38785

ID AAW38785 standard; peptide; 11 AA.

XX

AC AAW38785;

XX

DT 30-MAR-1998 (first entry)

XX

DE Delivery peptide used in peptide macromolecule complex.

XX

KW Delivery peptide; peptide-macromolecule complex; macromolecule delivery;

KW non-exchangeable lipophilic peptide; disease therapy; cell targeting.

XX

OS Synthetic.

XX

PN WO9725070-A2.

XX

PD 17-JUL-1997.

XX

PF 02-JAN-1997; 97WO-US000454.

XX

PR 08-JAN-1996; 96US-00584043.

XX

PA (BAYU ) BAYLOR COLLEGE MEDICINE.

XX

PI Smith LC, Sparrow JT, Hauer J, Mims MP;

XX

DR WPI; 1997-372622/34.

XX

PT New lipophilic peptide-macromolecule complexes - used for the delivery of

PT macromolecules to cells, particularly for gene therapy.

XX

PS Claim 6; Page 83; 106pp; English.

XX

CC This sequence represents a delivery peptide that can be used in the  
CC peptide-macromolecule complex of the invention. The peptide-macromolecule  
CC complex of the invention is for delivering a macromolecule into a cell,  
CC and comprises a non-exchangeable lipophilic peptide (LP) comprising a  
CC delivery peptide associated with a lipid moiety, where the delivery  
CC peptide portion of the LP is complexed to the macromolecule. The  
CC complexes can be used for the delivery of macromolecules such as nucleic  
CC acids, proteins, oligonucleotides, lipids or carbohydrates. They can be  
CC used to treat diseases by enhancing delivery of specific nucleic acid to  
CC the appropriate targeted cells. They can also be used to create

CC transformed cells as well as transgenic animals for assessing human  
CC disease in an animal model. They can also be used for livestock  
CC agricultural purposes. The complex is capable of transporting the  
CC macromolecule in a stable and condensed state and releasing the molecule  
CC into the cellular interior. The complex can bind with a cell surface  
CC receptor, lyse an endosome and target the nucleus of the cell

XX

SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KKKK 8

||||

Db 1 KKKK 4

RESULT 28

AAW38822

ID AAW38822 standard; peptide; 11 AA.

XX

AC AAW38822;

XX

DT 30-MAR-1998 (first entry)

XX

DE Delivery peptide used in peptide macromolecule complex.

XX

KW Delivery peptide; peptide-macromolecule complex; macromolecule delivery;

KW non-exchangeable lipophilic peptide; disease therapy; cell targeting.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Misc-difference 10

FT /note= "any amino acid"

XX

PN WO9725070-A2.

XX

PD 17-JUL-1997.

XX

PF 02-JAN-1997; 97WO-US000454.

XX

PR 08-JAN-1996; 96US-00584043.

XX

PA (BAYU ) BAYLOR COLLEGE MEDICINE.

XX

PI Smith LC, Sparrow JT, Hauer J, Mims MP;

XX

DR WPI; 1997-372622/34.

XX

PT New lipophilic peptide-macromolecule complexes - used for the delivery of  
PT macromolecules to cells, particularly for gene therapy.

XX

PS Claim 6; Page 63; 106pp; English.

XX

CC This sequence represents a delivery peptide that can be used in the

CC peptide-macromolecule complex of the invention. The peptide-macromolecule  
 CC complex of the invention is for delivering a macromolecule into a cell,  
 CC and comprises a non-exchangeable lipophilic peptide (LP) comprising a  
 CC delivery peptide associated with a lipid moiety, where the delivery  
 CC peptide portion of the LP is complexed to the macromolecule. The  
 CC complexes can be used for the delivery of macromolecules such as nucleic  
 CC acids, proteins, oligonucleotides, lipids or carbohydrates. They can be  
 CC used to treat diseases by enhancing delivery of specific nucleic acid to  
 CC the appropriate targeted cells. They can also be used to create  
 CC transformed cells as well as transgenic animals for assessing human  
 CC disease in an animal model. They can also be used for livestock  
 CC agricultural purposes. The complex is capable of transporting the  
 CC macromolecule in a stable and condensed state and releasing the molecule  
 CC into the cellular interior. The complex can bind with a cell surface  
 CC receptor, lyse an endosome and target the nucleus of the cell  
 XX  
 SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KKKK 8  
 ||||  
 Db 1 KKKK 4

# RESULT 29

AAW26074

ID AAW26074 standard; peptide; 11 AA.

XX

AC AAW26074;

XX

DT 28-OCT-1997 (first entry)

XX

DE M32 derivative of tenecin peptide fragment TED.

XX

KW Tenecin; antibiotic; antifungal peptide; Tenebrio molitor; chemotherapy;  
 KW systemic infection; pathogen.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 11

FT /note= "amidated"

XX

PN WO9702286-A1.

XX

PD 23-JAN-1997.

XX

PF 11-MAR-1996; 96WO-KR000034.

XX

PR 06-JUL-1995; 95KR-00019694.

PR 29-JAN-1996; 96KR-00001909.

PR 29-JAN-1996; 96KR-00001910.

PR 29-JAN-1996; 96KR-00001911.

XX

PA (MOGA-) MOGAM BIOTECHNOLOGY RES INST.  
 XX  
 PI Lee K, Hong S, Cho H, Lee B, Chung K, Yoon J, Oh J, Moon H;  
 XX  
 DR WPI; 1997-108913/10.  
 XX  
 PT Acid- or amide-form peptide(s) with antibacterial and antifungal activity  
 PT - used for chemotherapy of local and systemic infections caused by  
 PT pathogenic bacteria.  
 XX  
 PS Example 4; Page 17; 30pp; English.  
 XX  
 CC AAW26002-W26077 represent derivatives of the antibiotic fragments of  
 CC tenecin (see AAW26000) shown in AAW01830-W10835. AAW01830-W01835 are  
 CC amidated derivatives of antibiotic fragments of the wild type tenecin  
 CC sequence. These sequences are used as the antibacterial and antifungal  
 CC peptides of the invention. Tenecin is an antibacterial peptide isolated  
 CC from *Tenebrio molitor* larvae. Tenecin does have some drawbacks which  
 CC prevent it from practical use. Tenecin has a narrow spectrum of target  
 CC cells, and due to its large molecular size may provoke antigen-antibody  
 CC reactions in vivo, and is also unstable. The peptides can be used for the  
 CC development of antibacterial and antifungal agents for the chemotherapy  
 CC of local and systemic infections caused by pathogenic bacteria and/or  
 CC fungi and can be formulated into potent antibacterial and/or fungal  
 CC agents. The peptides have superior antibacterial and/or antifungal  
 CC activity, while causing no cytotoxicity. They do not give rise to lysing  
 CC of red blood cells. These peptides also have improved stability over the  
 CC wild type tenecin  
 XX  
 SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KKKK 8  
 ||||  
 Db 1 KKKK 4

RESULT 30  
 AAW16616  
 ID AAW16616 standard; peptide; 11 AA.  
 XX  
 AC AAW16616;  
 XX  
 DT 19-DEC-1997 (first entry)  
 XX  
 DE Phosphoinositide-3 kinase p110alpha conserved motif.  
 XX  
 KW Phosphoinositide 3 kinase; PI-3 kinase; wortmannin.  
 XX  
 OS Synthetic.  
 XX  
 PN W09715658-A1.  
 XX  
 PD 01-MAY-1997.

XX  
 PF 28-OCT-1996; 96WO-GB002614.  
 XX  
 PR 26-OCT-1995; 95GB-00021987.  
 XX  
 PA (LUDW-) LUDWIG INST CANCER RES.  
 XX  
 PI Wymann MP, Bulgarelli-Vela G, Panayotou G, Vanhaesebroeck B;  
 PI Zvelebil MJ, Waterfield MD;  
 XX  
 DR WPI; 1997-259013/23.  
 XX  
 PT Phospho:inositide 3 kinase wortmannin interaction site - to identify and  
 PT design ligands which regulate phospho:inositide 3 kinase activity.  
 XX  
 PS Disclosure; Page 32; 7lpp; English.  
 XX  
 CC A novel interaction site has been discovered on phosphoinositide 3 (PI-3)  
 CC kinase, or a homologue or analogue. The interaction site modulates the  
 CC activity of PI-3 kinase when exposed to a modulator, and has a molecular  
 CC shape adapted to interact with at least a part of the modulator so as to  
 CC modulate PI-3 kinase activity. The present sequence represents a  
 CC conserved motif (resembling K(X)nKXXX where n=3-7) in PI-3 kinase  
 CC p110alpha, that was found to bind phosphatidylinositol in gelsolin and so  
 CC might constitute a binding site for the 4,5-phosphates of the lipid. The  
 CC activity of PI-3 kinase can be regulated by altering, e.g. substituting a  
 CC different amino acid or deleting any of the features of the site. The  
 CC site may be used to identify or design novel ligands which regulate the  
 CC activity of PI-3 kinase by generating a molecular model of the wortmannin  
 CC inhibition site of PI-3 kinase, identifying or designing ligands which  
 CC interact with at least part of the site and optionally contacting the  
 CC putative ligand with PI-3 kinase and monitoring PI-3 kinase activity  
 XX  
 SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KKKK 8  
 ||||  
 Db 1 KKKK 4

RESULT 31  
 AAW86735  
 ID AAW86735 standard; peptide; 11 AA.  
 XX  
 AC AAW86735;  
 XX  
 DT 26-MAR-1999 (first entry)  
 XX  
 DE Anticoagulant peptide component.  
 XX  
 KW Anticoagulant; blood coagulation inhibitor; disulphide bond; catheter;  
 KW blood bag; dialysis membrane; artificial blood vessel.  
 XX

OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Cross-links 5  
 FT /note= "This residue is disulphide-bonded to Cys(7) of  
 FT the peptide KKHICICKK (see AAW86734)"  
 FT Cross-links 7  
 FT /note= "This residue is disulphide-bonded to Cys(5) of  
 FT the peptide KKHICICKK (see AAW86734)"  
 XX  
 PN JP11001493-A.  
 XX  
 PD 06-JAN-1999.  
 XX  
 PF 12-JUN-1997; 97JP-00172827.  
 XX  
 PR 12-JUN-1997; 97JP-00172827.  
 XX  
 PA (KURS ) KURARAY CO LTD.  
 XX  
 DR WPI; 1999-125476/11.  
 XX  
 PT New peptide which inhibits blood coagulation - useful in a pharmaceutical  
 PT material used as a catheter, blood vessel and blood dialysis membrane.  
 XX  
 PS Disclosure; Page 5; 18pp; Japanese.  
 XX  
 CC New inter- or intra-disulphide bonded peptides are disclosed which have  
 CC the formula A-X-Cys(1)-Y-Cys(2)-Z-B A'-X'-Cys(3)-Y'-Cys(4)-Z'-B' in  
 CC which: Cys(1) is disulphide-bonded to Cys(4); Cys(2) is disulphide-  
 CC bonded to Cys(3); A = H or forms a single bond together with B'; B = OH  
 CC or amino or forms a single bond together with A'; A' = H or forms a  
 CC single bond together with B; B' = OH or amino or forms a single bond  
 CC together with A; X and X' = peptide fragments composed of 3 to 13 amino  
 CC acid residues; Y and Y' = neutral or basic amino acid residues; and Z and  
 CC Z' = peptide fragments composed of 2 to 12 amino acid residues. These  
 CC peptides inhibit blood coagulation. They can be immobilised on the blood-  
 CC contacting surfaces of catheters, blood circuits, blood bags, blood  
 CC dialysis membranes, artificial blood vessels, etc. The present sequence  
 CC represents a specific example of the new peptides  
 XX  
 SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KKKK 8  
 ||||  
 Db 8 KKKK 11

RESULT 32  
 AAW77457  
 ID AAW77457 standard; peptide; 11 AA.  
 XX  
 AC AAW77457;

XX  
 DT 24-MAY-1999 (first entry)  
 XX  
 DE Lipophilic binding peptide.  
 XX  
 KW Lipophilic; binding; complex; gene therapy; cell targetting.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9850078-A1.  
 XX  
 PD 12-NOV-1998.  
 XX  
 PF 30-APR-1998; 98WO-US008849.  
 XX  
 PR 02-MAY-1997; 97US-0045295P.  
 XX  
 PA (GENE-) GENEMEDICINE INC.  
 PA (BAYU ) BAYLOR COLLEGE MEDICINE.  
 XX  
 PI Wadwha MS, Rolland A, Smith LC, Logan M, Sparrow JT;  
 XX  
 DR WPI; 1999-034689/03.  
 XX  
 PT New complex of macromolecule with lipophilic lytic and binding proteins -  
 PT used particularly for targetted delivery of nucleic acid to cells and  
 PT especially for gene therapy.  
 XX  
 PS Claim 9, 12; Page 81, 82; 98pp; English.  
 XX  
 CC The invention relates to new complexes for delivering a macromolecule to  
 CC cells in an organism. The complex comprises the macromolecule together  
 CC with either or both of a lipophilic lytic peptide and a lipophilic  
 CC binding peptide, both of these peptides including one or more hydrophobic  
 CC moieties. The present sequence is a preferred example of a lipophilic  
 CC binding peptide which can be used in the complex. The hydrophobic moiety  
 CC is preferably one or more palmitoyl or palmityl groups attached to the  
 CC amino groups of Lys residues in the peptide. The new complexes are  
 CC particularly used to deliver nucleic acids to specific tissues or cell  
 CC types. Alternatively the macromolecule may be a protein, peptide, lipid,  
 CC carbohydrate or peptidomimetic. Typical applications are gene therapy of  
 CC muscular dystrophy, ageing, osteoporosis, arthritis and lung cancer; as  
 CC vaccines; and for stimulating repair and regeneration of joints. The  
 CC peptides stabilise and condense the macromolecule. The binding peptide  
 CC allows targeting to selected cells, while the lytic peptide lyses  
 CC endosomes and so improves delivery of the macromolecule by preventing  
 CC degradation by lysosomes. The complex is effectively transported through  
 CC the cytoplasm to the nucleus  
 XX  
 SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KKKK 8  
 ||||

## RESULT 33

AAAY88559

ID AAY88559 standard; peptide; 11 AA.

XX

AC AAY88559;

XX

DT 07-AUG-2000 (first entry)

XX

DE NCAM Igl binding peptide 114 used as a control peptide.

XX

KW NCAM; neural cell adhesion molecule; Igl; immunoglobulin domain 1;

KW neurite outgrowth promoter; proliferation; nerve damage; sclerosis;

KW impaired myelination; stroke; Parkinson's disease; memory; schizophrenia;

KW Alzheimer's disease; diabetes mellitus; circadian clock; nephrosis;

KW treatment; prosthetic nerve guide; treatment; nervous system.

XX

OS Synthetic.

XX

PN WO200018801-A2.

XX

PD 06-APR-2000.

XX

PF 23-SEP-1999; 99WO-DK000500.

XX

PR 29-SEP-1998; 98DK-00001232.

PR 29-APR-1999; 99DK-00000592.

XX

PA (RONN/) RONN L C B.

PA (BOCK/) BOCK E.

PA (HOLM/) HOLM A.

PA (OLSE/) OLSEN M.

PA (OSTE/) OSTERGAARD S.

PA (JENS/) JENSEN P H.

PA (POUL/) POULSEN F M.

PA (SORO/) SOROKA V.

PA (RALE/) RALETS I.

PA (BERE/) BEREZIN V.

XX

PI Ronn LCB, Bock E, Holm A, Olsen M, Ostergaard S, Jensen PH;

PI Poulsen FM, Soroka V, Ralets I, Berezin V;

XX

DR WPI; 2000-293111/25.

XX

PT Compositions that bind neural cell adhesion molecules useful for treating

PT disorders of the nervous system and muscles e.g. Alzheimer's and

PT Parkinson's diseases.

XX

PS Example 5; Fig 7; 119pp; English.

XX

CC Neural cell adhesion molecule (NCAM) is a cellular adhesion molecule.

CC NCAM is found in three forms, two of which are transmembrane forms, while

CC the third is attached via a lipid anchor to the cell membrane. All three

CC NCAM forms have an extracellular structure consisting five immunoglobulin

CC domains (Ig domains). The Ig domains are numbered 1 to 5 from the N-



CC terminal. The invention relates to a compound containing a peptide which  
CC binds to the NCAM Ig1 domain. The compound binds to NCAM-Ig1/Ig2 domains,  
CC and is capable of stimulating or promoting neurite outgrowth from NCAM  
CC presenting cells, and is also capable of promoting the proliferation of  
CC NCAM presenting cells. The present sequence represents a control peptide  
CC used in the identification of those binding peptides which can be used in  
CC the compound. The compound may be used in the treatment of normal,  
CC degenerated or damaged NCAM presenting cells. The compound may in  
CC particular be used to treat diseases of the central and peripheral  
CC nervous systems such as post operative nerve damage, traumatic nerve  
CC damage, impaired myelination of nerve fibres, conditions resulting from a  
CC stroke, Parkinson's disease, Alzheimer's disease, dementias, sclerosis,  
CC nerve degeneration associated with diabetes mellitus, disorders affecting  
CC the circadian clock or neuro-muscular transmission and schizophrenia.  
CC Conditions affecting the muscles may also be treated with the compound,  
CC such as conditions associated with impaired function of neuromuscular  
CC connections (e.g. genetic or traumatic shock or traumatic atrophic muscle  
CC disorders). Conditions of the gonads, pancreas (e.g. diabetes mellitus  
CC types I and II), kidney (e.g. nephrosis), heart, liver and bowel may also  
CC be treated using the compound. The compound is used in a prosthetic nerve  
CC guide, and also to stimulate the ability to learn, and to stimulate the  
CC memory of a subject

XX

SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KKKK 8  
| | | |  
Db 7 KKKK 10

#### RESULT 34

AAAY88558

ID AAY88558 standard; peptide; 11 AA.

XX

AC AAY88558;

XX

DT 07-AUG-2000 (first entry)

XX

DE NCAM Ig1 binding peptide 121 used as a control peptide.

XX

KW NCAM; neural cell adhesion molecule; Ig1; immunoglobulin domain 1;  
KW neurite outgrowth promoter; proliferation; nerve damage; sclerosis;  
KW impaired myelination; stroke; Parkinson's disease; memory; schizophrenia;  
KW Alzheimer's disease; diabetes mellitus; circadian clock; nephrosis;  
KW treatment; prosthetic nerve guide; treatment; nervous system.

XX

OS Synthetic.

XX

PN WO200018801-A2.

XX

PD 06-APR-2000.

XX

PF 23-SEP-1999; 99WO-DK000500.

XX  
PR 29-SEP-1998; 98DK-00001232.  
PR 29-APR-1999; 99DK-00000592.  
XX  
PA (RONN/) RONN L C B.  
PA (BOCK/) BOCK E.  
PA (HOLM/) HOLM A.  
PA (OLSE/) OLSEN M.  
PA (OSTE/) OSTERGAARD S.  
PA (JENS/) JENSEN P H.  
PA (POUL/) POULSEN F M.  
PA (SORO/) SOROKA V.  
PA (RALE/) RALETS I.  
PA (BERE/) BEREZIN V.  
XX  
PI Ronn LCB, Bock E, Holm A, Olsen M, Ostergaard S, Jensen PH;  
PI Poulsen FM, Soroka V, Ralets I, Berezin V;  
XX  
DR WPI; 2000-293111/25.  
XX  
PT Compositions that bind neural cell adhesion molecules useful for treating  
PT disorders of the nervous system and muscles e.g. Alzheimer's and  
PT Parkinson's diseases.  
XX  
PS Example 5; Fig 7; 119pp; English.  
XX  
CC Neural cell adhesion molecule (NCAM) is a cellular adhesion molecule.  
CC NCAM is found in three forms, two of which are transmembrane forms, while  
CC the third is attached via a lipid anchor to the cell membrane. All three  
CC NCAM forms have an extracellular structure consisting five immunoglobulin  
CC domains (Ig domains). The Ig domains are numbered 1 to 5 from the N-  
CC terminal. The invention relates to a compound containing a peptide which  
CC binds to the NCAM Ig1 domain. The compound binds to NCAM-Ig1/Ig2 domains,  
CC and is capable of stimulating or promoting neurite outgrowth from NCAM  
CC presenting cells, and is also capable of promoting the proliferation of  
CC NCAM presenting cells. The present sequence represents a control peptide  
CC used in the identification of those binding peptides which can be used in  
CC the compound. The compound may be used in the treatment of normal,  
CC degenerated or damaged NCAM presenting cells. The compound may in  
CC particular be used to treat diseases of the central and peripheral  
CC nervous systems such as post operative nerve damage, traumatic nerve  
CC damage, impaired myelination of nerve fibres, conditions resulting from a  
CC stroke, Parkinson's disease, Alzheimer's disease, dementias, sclerosis,  
CC nerve degeneration associated with diabetes mellitus, disorders affecting  
CC the circadian clock or neuro-muscular transmission and schizophrenia.  
CC Conditions affecting the muscles may also be treated with the compound,  
CC such as conditions associated with impaired function of neuromuscular  
CC connections (e.g. genetic or traumatic shock or traumatic atrophic muscle  
CC disorders). Conditions of the gonads, pancreas (e.g. diabetes mellitus  
CC types I and II), kidney (e.g. nephrosis), heart, liver and bowel may also  
CC be treated using the compound. The compound is used in a prosthetic nerve  
CC guide, and also to stimulate the ability to learn, and to stimulate the  
CC memory of a subject  
XX  
SQ Sequence 11 AA;

Query Match

36.4%; Score 4; DB 3; Length 11;

Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KKKK 8  
||||  
Db 2 KKKK 5

RESULT 35

AAAY79943

ID AAY79943 standard; peptide; 11 AA.

XX

AC AAY79943;

XX

DT 11-MAY-2000 (first entry)

XX

DE Beta-amyloid hybrid peptide SEQ ID NO:8.

XX

KW Beta-amyloid; inhibitor; recognition element; hybrid; aggregation;

KW Alzheimer's disease; neuroprotective; nootropic.

XX

OS Homo sapiens.

OS Synthetic.

XX

PN US6022859-A.

XX

PD 08-FEB-2000.

XX

PF 14-NOV-1997; 97US-00970833.

XX

PR 15-NOV-1996; 96US-0030840P.

XX

PA (WISC ) WISCONSIN ALUMNI RES FOUND.

XX

PI Murphy RM, Kiessling LL;

XX

DR WPI; 2000-160387/14.

XX

PT Beta-amyloid inhibitor useful for treating Alzheimer's disease.

XX

PS Example; Col 7; 15pp; English.

XX

CC The present invention describes a beta-amyloid inhibitor peptide. Beta-

CC amyloid inhibitors have neuroprotective and nootropic properties. The

CC inhibitor peptides are useful for the treatment of Alzheimer's disease.

CC The present sequence represents a beta-amyloid hybrid peptide used in the  
CC exemplification of present invention

XX

SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 3; Length 11;

Best Local Similarity 100.0%; Pred. No. 1.2e+03;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KKKK 8  
||||  
Db 6 KKKK 9

RESULT 36

AAAY90160

ID AAY90160 standard; peptide; 11 AA.

XX

AC AAY90160;

XX

DT 06-AUG-2003 (revised)

DT 21-SEP-2000 (first entry)

XX

DE UPAR targeting sequence with spacers #10.

XX

KW Ligand epitope; UPAR; urokinase-type plasminogen activator receptor;  
KW adenovirus; hexon HVR5 loop; hexon HI loop; peripheral artery disease;  
KW recombinant adenovirus vector; tumour; restenosis; gene therapy; asthma;  
KW smooth muscle cell proliferation inhibitor; coronary artery disease;  
KW obesity; neurodegenerative disease; infection; autoimmune disease; HIV;  
KW thrombosis; diabetes; tropism-modified virus.

XX

OS Synthetic.

XX

PN WO200012738-A1.

XX

PD 09-MAR-2000.

XX

PF 27-AUG-1999; 99WO-IB001524.

XX

PR 27-AUG-1998; 98US-0098028P.

XX

PA (AVET ) AVENTIS PHARMA SA.

XX

PI Vigne E, Dedieu J, Latta M, Yeh P, Perricaudet M;

XX

DR WPI; 2000-256653/22.

XX

PT Urokinase-type plasminogen activator receptor (UPAR)-targeted adenovirus  
PT vectors having modified hexon HRV5 and HI loops and modified fiber  
PT proteins useful for targeted gene therapy to treat cancer or restenosis.

XX

PS Claim 15; Page 69; 128pp; English.

XX

CC This sequence represents a targeting sequence for UPAR, and is flanked by  
CC linkers. The invention relates to an adenovirus from which at least a  
CC part of the hexon HVR5 or HI loop is replaced with a binding peptide, or  
CC targeting sequence, flanked by connecting amino acid spacers, to  
CC functionally display its binding specificity at the capsid surface. The  
CC invention also relates to a recombinant adenovirus vector where a binding  
CC peptide, or targeting sequence, is connected to the C-terminus of the  
CC fiber by a connecting spacer, or linker, so as to functionally display  
CC its binding specificity at the capsid surface. The adenovirus or  
CC recombinant adenovirus vector can be used to preferentially express a  
CC gene in a target cell, especially a cell that expresses a UPAR. The  
CC targeted adenovirus vector preferably comprises a heterologous gene  
CC encoding a gene for treatment of a tumour or restenosis. The targeted  
CC adenovirus vector is useful for gene therapy treatment of a disease, and  
CC for manufacturing a medicine used in gene therapy treatment of a disease.

CC The viruses can also be used to inhibit smooth muscle cell proliferation,  
CC to treat peripheral artery diseases, coronary artery diseases, obesity,  
CC neurodegenerative diseases, infections, autoimmune diseases, asthma, HIV,  
CC thrombosis, and diabetes. The viruses are particularly targeted against a  
CC urokinase-type plasminogen activator receptor (UPAR). The adenoviruses  
CC are tropism-modified without adversely impacting productivity of the  
CC vectors. (Updated on 06-AUG-2003 to correct OS field.)

XX

SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 3; Length 11;

Best Local Similarity 100.0%; Pred. No. 1.2e+03;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KKKK 8

||||

Db 3 KKKK 6

#### RESULT 37

AAAY95530

ID AAY95530 standard; peptide; 11 AA.

XX

AC AAY95530;

XX

DT 10-OCT-2000 (first entry)

XX

DE Transactivator of transcription (Tat) peptide R52.

XX

KW Transactivator of transcription; Tat; HIV; AIDS; Kaposi's sarcoma;

KW antiviral; virucide; screening; retrovirus; antiretrovirus;

KW acetamidino saccharide; guanidino saccharide; aminoglycoside; antibiotic;

KW peptidomimetic.

XX

OS Human immunodeficiency virus.

OS Synthetic.

XX

PN WO200039139-A1.

XX

PD 06-JUL-2000.

XX

PF 28-DEC-1999; 99WO-IL000704.

XX

PR 28-DEC-1998; 98IL-00127773.

XX

PA (YEDA ) YEDA RES & DEV CO LTD.

XX

PI Lapidot A, Litovchick A, Evdokimov A;

XX

DR WPI; 2000-465729/40.

XX

PT Novel peptidomimetic conjugates of saccharides such as aminoglycoside

PT antibiotics with acetamidino and guanidino compounds useful for treating

PT HIV-infections, AIDS and AIDS manifestations such as Kaposi's sarcoma.

XX

PS Example 10; Page 27; 87pp; English.

XX

CC The present sequence is that of the model Tat (transactivator of  
CC transcription) peptide R52. Interaction of the HIV Tat with the  
CC transactivation responsive RNA (TAR) region of the HIV long terminal  
CC repeat regulates viral gene expression, and is an attractive target for  
CC drug design strategies. The invention is based on the discovery that by  
CC combining a carbohydrate skeleton, either a mono- or an oligosaccharide  
CC similar to aminoglycoside antibiotics, with side-chains of variable  
CC length bearing a guanidine moiety or a chemical group with a similar  
CC geometry and/or charge properties resembling peptide side chains, a new  
CC class of peptidomimetic TAR RNA binders is obtained that are anti-HIV  
CC compounds and suppress viral replication by inhibiting transactivation by  
CC Tat as well as by blocking viral entry to cells through chemokine  
CC receptor dependent mechanism. The present Tat peptide and a 31-nucleotide  
CC TAR RNA fragment (see AAA49983) were used in assays to screen for such  
CC compounds, which will be useful as antiviral, particularly  
CC antiretroviral, agents for treatment of HIV infection, AIDS and  
CC manifestations of AIDS, such as Kaposi's sarcoma

XX

SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KKKK 8  
| | | |  
Db 6 KKKK 9

#### RESULT 38

AAB29168

ID AAB29168 standard; peptide; 11 AA.

XX

AC AAB29168;

XX

DT 02-FEB-2001 (first entry)

XX

DE Peptide #12.

XX

KW Fork head associated; FHA; domain; transcriptional control;

KW DNA replication; DNA repair; cell cycle control.

XX

OS Unidentified.

XX

PN WO200057184-A2.

XX

PD 28-SEP-2000.

XX

PF 17-MAR-2000; 2000WO-GB001024.

XX

PR 19-MAR-1999; 99GB-00006432.

PR 28-JUN-1999; 99GB-00015075.

XX

PA (KUDO-) KUDOS PHARM LTD.

XX

PI Jackson SP, Durocher D;

XX

DR WPI; 2000-664872/64.

XX

PT Assays and screening methods based on direct interaction between FHA  
PT domains and phosphopeptides, useful for characterizing binding and to  
PT identify binding partners and modulators of FHA domain-phosphopeptide  
PT binding.

XX

PS Disclosure; Fig 2; 92pp; English.

XX

CC The present invention relates to assays and screening methods based on a  
CC direct interaction between fork head associated (FHA) domains and  
CC phosphorylated polypeptides, for characterizing the binding of these  
CC molecules. FHA peptides may be useful for treating medical conditions  
CC associated with defects in transcriptional control, DNA replication, DNA  
CC repair, cell cycle control or other cellular process. The method may  
CC provide valuable insights into checkpoint signalling, has important  
CC implications for the functions of other FHA domain-containing proteins  
CC and provides basis for new lines of therapy. The present sequence is a  
CC peptide used in the present invention

XX

SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GGKK 6

||||

Db 1 GGKK 4

#### RESULT 39

AAB50076

ID AAB50076 standard; peptide; 11 AA.

XX

AC AAB50076;

XX

DT 19-MAR-2001 (first entry)

XX

DE csk tyrosine kinase substrate.

XX

KW MLCK; MDCK; autoimmune disorder; Large NIK-Related Kinase 1;

KW wound healing; periodontal disease; inflammatory disease; tumour;

KW infection; allergy; LNRK1.

XX

OS Unidentified.

XX

PN WO200073468-A1.

XX

PD 07-DEC-2000.

XX

PF 26-MAY-2000; 2000WO-US014696.

XX

PR 28-MAY-1999; 99US-0136781P.

XX

PA (IMMV ) IMMUNEX CORP.

XX

PI Bird TA, Virca GD, Martin U, Anderson DM;  
 XX  
 DR WPI; 2001-061546/07.  
 XX  
 PT Novel murine and human kinase nucleic acids useful for treating  
 PT inflammations, infections, tumors, allergies, autoimmune diseases, and  
 PT for stimulating or suppressing immune responses.  
 XX  
 PS Example 5; Page 70; 106pp; English.  
 XX  
 CC The present invention relates to kinases (MDCK-1, -2 and -3 and MLSK-1  
 CC and -2; see AAB50053-B50057, and LNRK-1; see AAB50059). The kinases of  
 CC the present invention are useful for treating a variety of disorders  
 CC listed in the disclosure of the specification, including autoimmune  
 CC disorders, allergic reactions, myeloid or lymphoid cell deficiencies,  
 CC wound healing and tissue repair and replacement, burns, incisions and  
 CC ulcers, periodontal disease, inflammatory diseases, tumours and  
 CC bacterial, viral or fungal infection. The present sequence is a peptide  
 CC kinase substrate used in the present invention to investigate the  
 CC substrate specificity of MLSK-1  
 XX  
 SQ Sequence 11 AA;  
  
 Query Match 36.4%; Score 4; DB 4; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 Qy 5 KKKK 8  
 ||||  
 Db 1 KKKK 4

RESULT 40  
 AAM42176  
 ID AAM42176 standard; protein; 11 AA.  
 XX  
 AC AAM42176;  
 XX  
 DT 22-OCT-2001 (first entry)  
 XX  
 DE Human polypeptide SEQ ID NO 7107.  
 XX  
 KW Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;  
 KW peripheral nervous system; neuropathy; central nervous system; CNS;  
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;  
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;  
 KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;  
 KW leukaemia.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200153312-A1.  
 XX  
 PD 26-JUL-2001.  
 XX  
 PF 26-DEC-2000; 2000WO-US034263.  
 XX



PR 23-DEC-1999; 99US-00471275.  
PR 21-JAN-2000; 2000US-00488725.  
PR 25-APR-2000; 2000US-00552317.  
PR 20-JUN-2000; 2000US-00598042.  
PR 19-JUL-2000; 2000US-00620312.  
PR 03-AUG-2000; 2000US-00653450.  
PR 14-SEP-2000; 2000US-00662191.  
PR 19-OCT-2000; 2000US-00693036.  
PR 29-NOV-2000; 2000US-00727344.

XX

PA (HYSE-) HYSEQ INC.

XX

PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;  
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;  
PI Zhou P, Goodrich R, Drmanac RT;

XX

DR WPI; 2001-442253/47.

DR N-PSDB; AAI61332.

XX

PT Novel nucleic acids and polypeptides, useful for treating disorders such  
PT as central nervous system injuries.

XX

PS Example 2; SEQ ID NO 7107; 10078pp; English.

XX

CC The invention relates to human nucleic acids (AAI57798-AAI61369) and the  
CC encoded polypeptides (AAM38642-AAM42213) with nootropic,  
CC immunosuppressant and cytostatic activity. The polynucleotides are useful  
CC in gene therapy. A composition containing a polypeptide or polynucleotide  
CC of the invention may be used to treat diseases of the peripheral nervous  
CC system, such as peripheral nervous injuries, peripheral neuropathy and  
CC localised neuropathies and central nervous system diseases, such as  
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic  
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the  
CC utilisation of the activities such as: Immune system suppression,  
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic  
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,  
CC assays for receptor activity, arthritis and inflammation, leukaemias and  
CC C.N.S disorders. Note: The sequence data for this patent did not form  
CC part of the printed specification

XX

SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 4; Length 11;

Best Local Similarity 100.0%; Pred. No. 1.2e+03;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GKKK 7

||||

Db 8 GKKK 11

RESULT 41

AAB31770

ID AAB31770 standard; peptide; 11 AA.

XX

AC AAB31770;

XX

DT 30-APR-2001 (first entry)  
 XX  
 DE Amino acid sequence of a cross-linking peptide.  
 XX  
 KW Nucleic acid condensate; cationic linker; gene therapy.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200104135-A2.  
 XX  
 PD 18-JAN-2001.  
 XX  
 PF 13-JUL-2000; 2000WO-US019164.  
 XX  
 PR 13-JUL-1999; 99US-0143600P.  
 PR 05-OCT-1999; 99US-0157761P.  
 XX  
 PA (UNMI ) UNIV MICHIGAN.  
 XX  
 PI Rice KG, Adami RC, Mckenzie DL, Collard WT, Kwok K, Park Y;  
 PI Yang Y;  
 XX  
 DR WPI; 2001-168410/17.  
 XX  
 PT Compositions comprising nucleic acid condensates having a nucleic acid  
 PT bound to two low molecular weight cationic linkers, used in human gene  
 PT therapy, and diagnostics.  
 XX  
 PS Example 6; Page 108; 202pp; English.  
 XX  
 CC The specification describes a composition comprising a nucleic acid  
 CC condensate. This condensate comprises a nucleic acid bound to two low  
 CC molecular weight cationic linkers. The linkers are crosslinked to each  
 CC other by reaction with a low molecular weight dialdehyde. Alternatively,  
 CC the linkers each contain at least two thiol groups and are crosslinked by  
 CC reaction of the thiol groups. The low molecular weight carriers are  
 CC minimal in size, reduce toxicity, condense DNA into small particles, have  
 CC increased stability, and mediate effective gene expression in a target  
 CC tissue. The nucleic acid condensate is used for gene therapy,  
 CC particularly human gene therapy, and diagnostics. It is also used for  
 CC expressing nucleic acids in cells and providing a nucleic acid to an  
 CC animal. The present sequence represents a cross-linking peptide, which is  
 CC used as a linker in the composition of the invention. The peptide  
 CC condenses DNA  
 XX  
 SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 4; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KKKK 8  
 | | | |  
 Db 2 KKKK 5

RESULT 42

ABP19373

ID ABP19373 standard; peptide; 11 AA.

XX

AC ABP19373;

XX

DT 11-SEP-2003 (revised)

DT 15-JUL-2002 (first entry)

XX

DE HIV B62 super motif pol peptide #379.

XX

KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;

KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;

KW vaccine; HIV infection; immunisation; virucide.

XX

OS Human immunodeficiency virus 1.

XX

PN WO200124810-A1.

XX

PD 12-APR-2001.

XX

PF 05-OCT-2000; 2000WO-US027766.

XX

PR 05-OCT-1999; 99US-00412863.

XX

PA (EPIM-) EPIMMUNE INC.

XX

PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;

PI Baker DM, Celis E, Kubo RT, Grey HM;

XX

DR WPI; 2001-354887/37.

XX

PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)

PT peptide groups, useful for vaccinating against HIV-1.

XX

PS Claim 32; Page 265; 448pp; English.

XX

CC The present invention describes a composition (I) comprising a prepared  
CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
CC sequence selected from 51 defined amino acid sequences (ABL25347 to  
CC ABP25397). (I) has virucide activity and can be used in vaccines. (I) may  
CC be used for immunising subjects against HIV-1 infections. The use of  
CC group-based vaccines has several advantages over traditional vaccines,  
CC particularly when compared to the use of whole antigens in vaccine  
CC compositions. There is evidence that the immune response to whole  
CC antigens is directed largely toward variable regions of the antigen,  
CC allowing for immune escape due to mutations. The groups for inclusion in  
CC an group-based vaccine may be selected from conserved regions of viral or  
CC tumour-associated antigens, which therefore reduces the likelihood of  
CC escape mutants. Furthermore, immunosuppressive groups that may be present  
CC in whole antigens can be avoided with the use of group-based vaccines. An  
CC additional advantage of an group-based vaccine approach is the ability to  
CC combine selected groups (CTL and HTL), and further, to modify the  
CC composition of the groups, achieving, for example, enhanced  
CC immunogenicity. Accordingly, the immune response can be modulated, as  
CC appropriate, for the target disease. Similar engineering of the response  
CC is not possible with traditional approaches. ABP11501 to ABP25412  
CC represent peptide sequences used in the exemplification of the present

CC invention. (Updated on 11-SEP-2003 to standardise OS field)  
XX  
SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KKKK 8  
|||  
Db 6 KKKK 9

RESULT 43

ABP13804

ID ABP13804 standard; peptide; 11 AA.

XX

AC ABP13804;

XX

DT 11-SEP-2003 (revised)

DT 15-JUL-2002 (first entry)

XX

DE HIV A02 super motif pol peptide #719.

XX

KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;  
KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;  
KW vaccine; HIV infection; immunisation; virucide.

XX

OS Human immunodeficiency virus 1.

XX

PN WO200124810-A1.

XX

PD 12-APR-2001.

XX

PF 05-OCT-2000; 2000WO-US027766.

XX

PR 05-OCT-1999; 99US-00412863.

XX

PA (EPIM-) EPIMMUNE INC.

XX

PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;

PI Baker DM, Celis E, Kubo RT, Grey HM;

XX

DR WPI; 2001-354887/37.

XX

PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)  
PT peptide groups, useful for vaccinating against HIV-1.

XX

PS Claim 32; Page 151; 448pp; English.

XX

CC The present invention describes a composition (I) comprising a prepared  
CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
CC sequence selected from 51 defined amino acid sequences (ABL25347 to  
CC ABP25397). (I) has virucide activity and can be used in vaccines. (I) may  
CC be used for immunising subjects against HIV-1 infections. The use of  
CC group-based vaccines has several advantages over traditional vaccines,  
CC particularly when compared to the use of whole antigens in vaccine

CC compositions. There is evidence that the immune response to whole  
 CC antigens is directed largely toward variable regions of the antigen,  
 CC allowing for immune escape due to mutations. The groups for inclusion in  
 CC an group-based vaccine may be selected from conserved regions of viral or  
 CC tumour-associated antigens, which therefore reduces the likelihood of  
 CC escape mutants. Furthermore, immunosuppressive groups that may be present  
 CC in whole antigens can be avoided with the use of group-based vaccines. An  
 CC additional advantage of an group-based vaccine approach is the ability to  
 CC combine selected groups (CTL and HTL), and further, to modify the  
 CC composition of the groups, achieving, for example, enhanced  
 CC immunogenicity. Accordingly, the immune response can be modulated, as  
 CC appropriate, for the target disease. Similar engineering of the response  
 CC is not possible with traditional approaches. ABP11501 to ABP25412  
 CC represent peptide sequences used in the exemplification of the present  
 CC invention. (Updated on 11-SEP-2003 to standardise OS field)

XX

SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 4; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KKKK 8  
 ||||  
 Db 5 KKKK 8

#### RESULT 44

ABP17176

ID ABP17176 standard; peptide; 11 AA.

XX

AC ABP17176;

XX

DT 11-SEP-2003 (revised)

DT 15-JUL-2002 (first entry)

XX

DE HIV B27 super motif gag peptide #52.

XX

KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;  
 KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;  
 KW vaccine; HIV infection; immunisation; virucide.

XX

OS Human immunodeficiency virus 1.

XX

PN WO200124810-A1.

XX

PD 12-APR-2001.

XX

PF 05-OCT-2000; 2000WO-US027766.

XX

PR 05-OCT-1999; 99US-00412863.

XX

PA (EPIM-) EPIMMUNE INC.

XX

PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;

PI Baker DM, Celis E, Kubo RT, Grey HM;

XX

DR WPI; 2001-354887/37.

XX

PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)  
PT peptide groups, useful for vaccinating against HIV-1.

XX

PS Claim 32; Page 221; 448pp; English.

XX

CC The present invention describes a composition (I) comprising a prepared  
CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
CC sequence selected from 51 defined amino acid sequences (ABL25347 to  
CC ABP25397). (I) has virucide activity and can be used in vaccines. (I) may  
CC be used for immunising subjects against HIV-1 infections. The use of  
CC group-based vaccines has several advantages over traditional vaccines,  
CC particularly when compared to the use of whole antigens in vaccine  
CC compositions. There is evidence that the immune response to whole  
CC antigens is directed largely toward variable regions of the antigen,  
CC allowing for immune escape due to mutations. The groups for inclusion in  
CC an group-based vaccine may be selected from conserved regions of viral or  
CC tumour-associated antigens, which therefore reduces the likelihood of  
CC escape mutants. Furthermore, immunosuppressive groups that may be present  
CC in whole antigens can be avoided with the use of group-based vaccines. An  
CC additional advantage of an group-based vaccine approach is the ability to  
CC combine selected groups (CTL and HTL), and further, to modify the  
CC composition of the groups, achieving, for example, enhanced  
CC immunogenicity. Accordingly, the immune response can be modulated, as  
CC appropriate, for the target disease. Similar engineering of the response  
CC is not possible with traditional approaches. ABP11501 to ABP25412  
CC represent peptide sequences used in the exemplification of the present  
CC invention. (Updated on 11-SEP-2003 to standardise OS field)

XX

SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GKKK 7  
|||  
Db 1 GKKK 4

RESULT 45

ABP13805

ID ABP13805 standard; peptide; 11 AA.

XX

AC ABP13805;

XX

DT 11-SEP-2003 (revised)

DT 15-JUL-2002 (first entry)

XX

DE HIV A02 super motif pol peptide #720.

XX

KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;  
KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;  
KW vaccine; HIV infection; immunisation; virucide.

XX

OS Human immunodeficiency virus 1.

XX  
 PN WO200124810-A1.  
 XX  
 PD 12-APR-2001.  
 XX  
 PF 05-OCT-2000; 2000WO-US027766.  
 XX  
 PR 05-OCT-1999; 99US-00412863.  
 XX  
 PA (EPIM-) EPIMMUNE INC.  
 XX  
 PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;  
 PI Baker DM, Celis E, Kubo RT, Grey HM;  
 XX  
 DR WPI; 2001-354887/37.  
 XX  
 PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)  
 PT peptide groups, useful for vaccinating against HIV-1.  
 XX  
 PS Claim 32; Page 151; 448pp; English.  
 XX  
 CC The present invention describes a composition (I) comprising a prepared  
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
 CC sequence selected from 51 defined amino acid sequences (ABL25347 to  
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I) may  
 CC be used for immunising subjects against HIV-1 infections. The use of  
 CC group-based vaccines has several advantages over traditional vaccines,  
 CC particularly when compared to the use of whole antigens in vaccine  
 CC compositions. There is evidence that the immune response to whole  
 CC antigens is directed largely toward variable regions of the antigen,  
 CC allowing for immune escape due to mutations. The groups for inclusion in  
 CC an group-based vaccine may be selected from conserved regions of viral or  
 CC tumour-associated antigens, which therefore reduces the likelihood of  
 CC escape mutants. Furthermore, immunosuppressive groups that may be present  
 CC in whole antigens can be avoided with the use of group-based vaccines. An  
 CC additional advantage of an group-based vaccine approach is the ability to  
 CC combine selected groups (CTL and HTL), and further, to modify the  
 CC composition of the groups, achieving, for example, enhanced  
 CC immunogenicity. Accordingly, the immune response can be modulated, as  
 CC appropriate, for the target disease. Similar engineering of the response  
 CC is not possible with traditional approaches. ABP11501 to ABP25412  
 CC represent peptide sequences used in the exemplification of the present  
 CC invention. (Updated on 11-SEP-2003 to standardise OS field)  
 XX  
 SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 4; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KKKK 8  
 ||||  
 Db 3 KKKK 6

RESULT 46  
 AAU76079

ID AAU76079 standard; peptide; 11 AA.  
XX  
AC AAU76079;  
XX  
DT 08-MAY-2002 (first entry)  
XX  
DE Nociceptin-like peptide conjugate 16.  
XX  
KW Nociceptin; opioid receptor-like 1; ORL1; hyponatraemia;  
KW coronary heart failure; diuretic therapy; thiazide; loop diuretic;  
KW water diuresis; congestive heart failure; liver cirrhosis;  
KW nephrotic syndrome; hypertension; multiple organ failure;  
KW acute renal failure; hypokalaemia; oedema.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Modified-site 1  
FT /note= "Cys is hydrogenated"  
FT Modified-site 11  
FT /note= "Lys is amidated"  
XX  
PN WO200198324-A1.  
XX  
PD 27-DEC-2001.  
XX  
PF 15-JUN-2001; 2001WO-US019113.  
XX  
PR 16-JUN-2000; 2000DK-00000944.  
PR 05-OCT-2000; 2000DK-00001485.  
PR 06-DEC-2000; 2000US-0251671P.  
PR 13-JUN-2001; 2001WO-US041008.  
XX  
PA (ZEAL-) ZEALAND PHARM AS.  
XX  
PI Larsen BD, Petersen JS, Kapusta DR, Harlow KW;  
XX  
DR WPI; 2002-171551/22.  
XX  
PT New peptide conjugate useful for preparing medicament for treating  
PT congestive heart failure, liver cirrhosis, nephrotic syndrome and  
PT hypertension comprises modified N and/or C terminals.  
XX  
PS Example 17; Page 46; 72pp; English.  
XX  
CC The invention relates to a peptide conjugate of the general formula (A).  
CC  $R_1-Z-X-Z'-R_2$  (A); where X = a hexapeptide of formula (B);  $A^1-A^2-A^3-$   
CC  $A^4-A^5-A^6$  (B);  $A^1 = R, K, \text{ or } H$ ;  $A^2 = Y, W, \text{ or } F$ ;  $A^3 = Y, N, W \text{ or } F$ ;  
CC  $A^4 = K, R \text{ or } H$ ;  $A^5 = F, Y, W, L, V \text{ or } I$ ; and  $A^6 = R, K \text{ or } H$ . Each  
CC amino acid residue in the hexapeptide may be in the L or D form, Z and Z'  
CC = a charged peptide chain of 4-20 amino acid residues having the D or L  
CC configuration or is missing provided that not both of Z and Z' are  
CC missing;  $R^1 = H \text{ or an acyl group}$ ; and  $R^2 = NR^3R^4 \text{ or } OH$ ;  $R^3, R^4 = H,$   
CC C(1-6)alkoxy, aryloxy or a lower alkyl as defined, where the conjugate  
CC being optionally further linked to a transport moiety, and salts,  
CC hydrates and their solvates, and C-terminally amidated or their  
CC esterified derivatives with suitable organic or inorganic acids.



CC Alternatively, the conjugate has a general formula (C). R<sub>1</sub>-X-Z'-R<sub>2</sub> (C),  
 CC Where R<sub>1</sub>, X, Z' and R<sub>2</sub> are same as defined in formula A; and salts,  
 CC hydrates and their solvates, and C-terminally amidated or their  
 CC esterified derivatives with suitable organic or inorganic acids. The  
 CC conjugate may also be linked to counterions selected from anions,  
 CC preferably CH<sub>3</sub>COO<sup>-</sup>, CF<sub>3</sub>COO<sup>-</sup>, Cl<sup>-</sup>, SO<sub>3</sub><sup>2-</sup>, maleate or oleate. Also  
 CC included are nucleic acids encoding the peptides, a host cell comprising/  
 CC expressing the peptides and antibodies against the peptides. The peptides  
 CC and conjugates are useful for the preparation of a medicament for the  
 CC treatment and/or prevention of hypotatraemia which is preferably  
 CC associated with heart failure, or with intensive diuretic therapy with  
 CC thiazides and/or loop diuretics, water diuresis, congestive heart  
 CC failure, liver cirrhosis, nephrotic syndrome and hypertension, multiple  
 CC organ failure, acute renal failure, disease states associated with  
 CC elevated tone of nociceptin, hypokalaemia, oedema associated with  
 CC coronary heart failure. The hexapeptides are in part based on the  
 CC sequence of formula (RK)YY(RK)(WI)(RK), a partial agonist of the  
 CC nociceptin, opioid receptor-like one (ORL1) which can be used to raise  
 CC antibodies against the conjugates. The present sequence is a peptide  
 CC conjugate of the invention  
 XX  
 SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 5; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KKKK 8  
 ||||  
 Db 6 KKKK 9

# RESULT 47

AAU76110

ID AAU76110 standard; peptide; 11 AA.

XX

AC AAU76110;

XX

DT 08-MAY-2002 (first entry)

XX

DE Nociceptin-like peptide conjugate compound 12.

XX

KW Nociceptin; opioid receptor-like 1; ORL1; hypotatraemia;

KW coronary heart failure; diuretic therapy; thiazide; loop diuretic;

KW water diuresis; congestive heart failure; liver cirrhosis;

KW nephrotic syndrome; hypertension; multiple organ failure;

KW acute renal failure; hypokalaemia; oedema.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "Arg is acetylated"

FT Modified-site 11

FT /note= "Lys is amidated"

XX

PN WO200198324-A1.

XX  
PD 27-DEC-2001.  
XX  
PF 15-JUN-2001; 2001WO-US019113.  
XX  
PR 16-JUN-2000; 2000DK-00000944.  
PR 05-OCT-2000; 2000DK-00001485.  
PR 06-DEC-2000; 2000US-0251671P.  
PR 13-JUN-2001; 2001WO-US041008.  
XX  
PA (ZEAL-) ZEALAND PHARM AS.  
XX  
PI Larsen BD, Petersen JS, Kapusta DR, Harlow KW;  
XX  
DR WPI; 2002-171551/22.  
XX  
PT New peptide conjugate useful for preparing medicament for treating  
PT congestive heart failure, liver cirrhosis, nephrotic syndrome and  
PT hypertension comprises modified N and/or C terminals.  
XX  
PS Claim 19; Page 52; 72pp; English.  
XX  
CC The invention relates to a peptide conjugate of the general formula (A).  
CC  $R_1-Z-X-Z'-R_2$  (A); where X = a hexapeptide of formula (B);  $A^1-A^2-A^3-$   
CC  $A^4-A^5-A^6$  (B);  $A^1 = R, K, \text{ or } H$ ;  $A^2 = Y, W, \text{ or } F$ ;  $A^3 = Y, N, W \text{ or } F$ ;  
CC  $A^4 = K, R \text{ or } H$ ;  $A^5 = F, Y, W, L, V \text{ or } I$ ; and  $A^6 = R, K \text{ or } H$ . Each  
CC amino acid residue in the hexapeptide may be in the L or D form, Z and Z'  
CC = a charged peptide chain of 4-20 amino acid residues having the D or L  
CC configuration or is missing provided that not both of Z and Z' are  
CC missing;  $R^1 = H$  or an acyl group; and  $R^2 = NR^3R^4$  or OH;  $R^3, R^4 = H,$   
CC C(1-6)alkoxy, aryloxy or a lower alkyl as defined, where the conjugate  
CC being optionally further linked to a transport moiety, and salts,  
CC hydrates and their solvates, and C-terminally amidated or their  
CC esterified derivatives with suitable organic or inorganic acids.  
CC Alternatively, the conjugate has a general formula (C).  $R_1-X-Z'-R_2$  (C),  
CC Where  $R_1, X, Z'$  and  $R_2$  are same as defined in formula A; and salts,  
CC hydrates and their solvates, and C-terminally amidated or their  
CC esterified derivatives with suitable organic or inorganic acids. The  
CC conjugate may also be linked to counterions selected from anions,  
CC preferably  $CH_3COO^-$ ,  $CF_3COO^-$ ,  $Cl^-$ ,  $SO_3^{2-}$ , maleate or oleate. Also  
CC included are nucleic acids encoding the peptides, a host cell comprising/  
CC expressing the peptides and antibodies against the peptides. The peptides  
CC and conjugates are useful for the preparation of a medicament for the  
CC treatment and/or prevention of hypotraemia which is preferably  
CC associated with heart failure, or with intensive diuretic therapy with  
CC thiazides and/or loop diuretics, water diuresis, congestive heart  
CC failure, liver cirrhosis, nephrotic syndrome and hypertension, multiple  
CC organ failure, acute renal failure, disease states associated with  
CC elevated tone of nociceptin, hypokalaemia, oedema associated with  
CC coronary heart failure. The hexapeptides are in part based on the  
CC sequence of formula (RK)YY(RK)(WI)(RK), a partial agonist of the  
CC nociceptin, opioid receptor-like one (ORL1) which can be used to raise  
CC antibodies against the conjugates. The present sequence is a peptide  
CC conjugate of the invention  
XX  
SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 5; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KKKK 8  
    ||||  
Db 6 KKKK 9

RESULT 48

AAU96727

ID AAU96727 standard; peptide; 11 AA.

XX

AC AAU96727;

XX

DT 30-JUL-2002 (first entry)

XX

DE Molecular marker for electrophoresis #12.

XX

KW Molecular marker; electrophoresis; protein characterisation;

KW two dimensional gel electrophoresis; molecular weight; isoelectric point.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "Cysteine or Protein with C-terminal thioester"

FT Modified-site 2

FT /note= "N alpha-(9-fluorenylmethoxy-carbonyl)-N epsilon-tetramethylrhodamine"

FT Modified-site 3

FT /note= "N alpha-(9-fluorenylmethoxy-carbonyl)-N epsilon-tetramethylrhodamine"

FT Modified-site 4

FT /note= "N alpha-(9-fluorenylmethoxy-carbonyl)-N epsilon-tetramethylrhodamine"

FT Modified-site 5

FT /note= "N alpha-(9-fluorenylmethoxy-carbonyl)-N epsilon-tetramethylrhodamine"

FT Modified-site 11

FT /note= "Thioester-linked histidine"

XX

PN WO200213848-A1.

XX

PD 21-FEB-2002.

XX

PF 13-AUG-2001; 2001WO-US025276.

XX

PR 11-AUG-2000; 2000US-0224345P.

XX

PA (INVI-) INVITROGEN CORP.

XX

PI Tadayoni-Rebek M, Amshey JW, Rooney R;

XX

DR WPI; 2002-382623/41.

XX

PT Marker molecule useful for separation of at least one molecule e.g.

PT protein in a gel electrophoresis comprises a labeled molecule attached  
PT via a linker or a bond to a protein or nucleic acid.  
XX  
PS Disclosure; Fig 4; 64pp; English.  
XX  
CC The invention describes marker molecules comprising a labeled molecule  
CC attached via a linker or a bond to a protein or nucleic acid. The  
CC molecules are useful: when separating at least one molecule present in a  
CC sample; for characterisation of at least one protein or molecule; in  
CC protein marker kits; in two dimensional gel electrophoresis; to analyse  
CC at least one protein to determine their molecular weights and the  
CC isoelectric point; and for identifying physical properties of molecular  
CC species (preferably deoxyribonucleic acid, ribonucleic acid, polypeptide  
CC and protein) separated the use of electrophoretic systems. The marker  
CC molecules will generally separate to give narrow, sharp bands or spots  
CC under electrophoretic conditions and are highly homogeneous, visible  
CC (preferably coloured) molecular markers that are compatible with  
CC commercially available separation technique, especially the techniques  
CC that separate proteins on the basis of charge and/or molecular weight.  
CC This sequence represents a molecular marker for identifying physical  
CC properties of molecular species separated by the use of electrophoretic  
CC systems  
XX  
SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 5; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KKKK 8  
| | | |  
Db 2 KKKK 5

RESULT 49  
ABB74600  
ID ABB74600 standard; peptide; 11 AA.  
XX  
AC ABB74600;  
XX  
DT 18-APR-2002 (first entry)  
XX  
DE Transcription factor nuclear localisation signal peptide SEQ ID NO:364.  
XX  
KW Fusogenic; nuclear localisation signal; NLS; encapsulation; lipogene;  
KW liposome; micelle; karyophilic; cytostatic; antitumour; solid tumour;  
KW peptide-lipid-polynucleotide complex; neoplastic disease; gene therapy;  
KW breast carcinoma; prostate carcinoma.  
XX  
OS Homo sapiens.  
XX  
PN WO200193836-A2.  
XX  
PD 13-DEC-2001.  
XX  
PF 08-JUN-2001; 2001WO-US018657.  
XX

PR 09-JUN-2000; 2000US-0210925P.

XX

PA (BOUL/) BOULIKAS T.

XX

PI Boulikas T;

XX

DR WPI; 2002-164295/21.

XX

PT Encapsulation of plasmid DNA (Lipogenes) and therapeutic agents with  
PT nuclear localization signal/fusogenic peptide conjugates into targeted  
PT liposome complexes.

XX

PS Claim 14; Page 76; 107pp; English.

XX

CC The present invention describes a method for producing micelles with  
CC entrapped therapeutic agents. The method comprises: (1) combining  
CC negatively charged agent with a cationic lipid in a ratio where 30-90 %  
CC of the negatively charged atoms are neutralised by positive charges on  
CC lipid molecules to form an electrostatic micelle complex in 20-80 %  
CC ethanol; and (2) combining the micelle complex of (a) with fusogenic-  
CC karyophilic peptide conjugates in a 0.0-0.3 ratio, therefore producing  
CC micelles with entrapped therapeutic agents. Also described is a method  
CC for delivering a therapeutic agent in vivo, comprising the administration  
CC of the micelle. ABB74256 to ABB74858 represent specifically claimed  
CC nuclear localisation signal (NLS) peptides for use in the method as the  
CC fusogenic-karyophilic peptides. The micelles produced can have cytostatic  
CC and antitumour activities. The peptide-lipid-polynucleotide complexes  
CC produced are useful for inhibiting the progression of neoplastic  
CC diseases. The invention relates to the field of gene therapy and is  
CC directed toward methods for producing peptide-lipid-polynucleotide  
CC complexes suitable for delivery of polynucleotides. The encapsulated  
CC molecules display therapeutic efficacy in eradicating solid tumours  
CC including but not limited to breast carcinoma or prostate carcinoma.  
CC ABB74235 to ABB74255 are used in the exemplification of the present  
CC invention

XX

SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 5; Length 11;

Best Local Similarity 100.0%; Pred. No. 1.2e+03;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GKKK 7

||||

Db 1 GKKK 4

RESULT 50

ABB74327

ID ABB74327 standard; peptide; 11 AA.

XX

AC ABB74327;

XX

DT 18-APR-2002 (first entry)

XX

DE Bipartite/split nuclear localisation signal peptide SEQ ID NO:91.

XX

KW Fusogenic; nuclear localisation signal; NLS; encapsulation; lipogene;  
KW liposome; micelle; karyophilic; cytostatic; antitumour; solid tumour;  
KW peptide-lipid-polynucleotide complex; neoplastic disease; gene therapy;  
KW breast carcinoma; prostate carcinoma.

XX

OS Synthetic.

XX

PN WO200193836-A2.

XX

PD 13-DEC-2001.

XX

PF 08-JUN-2001; 2001WO-US018657.

XX

PR 09-JUN-2000; 2000US-0210925P.

XX

PA (BOUL/) BOULIKAS T.

XX

PI Boulikas T;

XX

DR WPI; 2002-164295/21.

XX

PT Encapsulation of plasmid DNA (Lipogenes) and therapeutic agents with  
PT nuclear localization signal/fusogenic peptide conjugates into targeted  
PT liposome complexes.

XX

PS Claim 14; Page 58; 107pp; English.

XX

CC The present invention describes a method for producing micelles with  
CC entrapped therapeutic agents. The method comprises: (1) combining  
CC negatively charged agent with a cationic lipid in a ratio where 30-90 %  
CC of the negatively charged atoms are neutralised by positive charges on  
CC lipid molecules to form an electrostatic micelle complex in 20-80 %  
CC ethanol; and (2) combining the micelle complex of (a) with fusogenic-  
CC karyophilic peptide conjugates in a 0.0-0.3 ratio, therefore producing  
CC micelles with entrapped therapeutic agents. Also described is a method  
CC for delivering a therapeutic agent in vivo, comprising the administration  
CC of the micelle. ABB74256 to ABB74858 represent specifically claimed  
CC nuclear localisation signal (NLS) peptides for use in the method as the  
CC fusogenic-karyophilic peptides. The micelles produced can have cytostatic  
CC and antitumour activities. The peptide-lipid-polynucleotide complexes  
CC produced are useful for inhibiting the progression of neoplastic  
CC diseases. The invention relates to the field of gene therapy and is  
CC directed toward methods for producing peptide-lipid-polynucleotide  
CC complexes suitable for delivery of polynucleotides. The encapsulated  
CC molecules display therapeutic efficacy in eradicating solid tumours  
CC including but not limited to breast carcinoma or prostate carcinoma.  
CC ABB74235 to ABB74255 are used in the exemplification of the present  
CC invention

XX

SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 5; Length 11;

Best Local Similarity 100.0%; Pred. No. 1.2e+03;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy

5 KKKK 8

||||

## RESULT 51

ABG67641

ID ABG67641 standard; peptide; 11 AA.

XX

AC ABG67641;

XX

DT 07-OCT-2002 (first entry)

XX

DE Human ADPI tryptic digest peptide #350.

XX

KW Human; Alzheimer's disease; AD; brain tissue; ADF; ADPI;

KW Alzheimer's disease-associated feature; neuroprotective;

KW Alzheimer's disease-associated protein isoform; nootropic;

KW ADPI tryptic digest peptide.

XX

OS Homo sapiens.

XX

PN WO200246767-A2.

XX

PD 13-JUN-2002.

XX

PF 29-NOV-2001; 2001WO-GB005289.

XX

PR 08-DEC-2000; 2000US-0254431P.

XX

PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.

XX

PI Herath HMAc, Parekh RB, Rohlf C;

XX

DR WPI; 2002-508575/54.

XX

PT Screening, diagnosis or prognosis of Alzheimer's disease in subject,  
PT comprises detecting Alzheimer disease-associated features or Alzheimer  
PT disease-associated protein isoforms in brain tissue from the subject.

XX

PS Claim 7; Page 84; 427pp; English.

XX

CC The present invention relates to methods and compositions for the  
CC screening, diagnosis or prognosis of Alzheimer's disease (AD) in a  
CC subject. The method comprises analysing a sample of brain tissue from a  
CC subject by 2D electrophoresis to generate a 2D array of Alzheimer's  
CC disease-associated features (ADFs), whose relative abundance correlates  
CC with the presence, absence, stage or severity of AD and comparing the  
CC abundance of each feature with the abundance of that chosen feature in  
CC brain tissue from persons free from AD. The invention also describes  
CC Alzheimer's disease-associated protein isoforms (ADPIs) detectable in  
CC brain tissue. The methods and compositions of the invention are useful  
CC for the screening, diagnosis or prognosis of AD in a subject, for  
CC determining the stage or severity of AD in a subject, for identifying a  
CC subject at risk of developing AD, or for monitoring the effect of therapy  
CC administered to a subject having AD. Antibodies capable of binding to  
CC ADPIs are useful for treating or preventing AD, and for determining the  
CC efficacy of a given treatment regime. An agent that modulates the  
CC activity of ADPI is useful in the manufacture of a medicament for the

CC treatment or prevention of AD in a subject. ABG67292-ABG68038 represent  
CC human ADPI tryptic digest peptides  
XX  
SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 5; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEGG 4  
| | | |  
Db 3 AEGG 6

RESULT 52

ABG70612

ID ABG70612 standard; peptide; 11 AA.

XX

AC ABG70612;

XX

DT 10-DEC-2002 (first entry)

XX

DE [Lys]11 11 HBr peptide.

XX

KW Active agent delivery system; degradation; controlled release; stability;

KW stomach; conformational protection; digestion;

KW intestinal tract absorption.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 11

FT /note= "Modified by 11 HBr"

XX

PN US2002099013-A1.

XX

PD 25-JUL-2002.

XX

PF 22-AUG-2001; 2001US-00933708.

XX

PR 14-NOV-2000; 2000US-0247556P.

PR 14-NOV-2000; 2000US-0247558P.

PR 14-NOV-2000; 2000US-0247559P.

PR 14-NOV-2000; 2000US-0247560P.

PR 14-NOV-2000; 2000US-0247561P.

PR 14-NOV-2000; 2000US-0247594P.

PR 14-NOV-2000; 2000US-0247595P.

PR 14-NOV-2000; 2000US-0247606P.

PR 14-NOV-2000; 2000US-0247607P.

PR 14-NOV-2000; 2000US-0247608P.

PR 14-NOV-2000; 2000US-0247609P.

PR 14-NOV-2000; 2000US-0247610P.

PR 14-NOV-2000; 2000US-0247611P.

PR 14-NOV-2000; 2000US-0247612P.

PR 14-NOV-2000; 2000US-0247613P.

PR 14-NOV-2000; 2000US-0247614P.

PR 14-NOV-2000; 2000US-0247615P.



PR 14-NOV-2000; 2000US-0247616P.  
PR 14-NOV-2000; 2000US-0247617P.  
PR 14-NOV-2000; 2000US-0247620P.  
PR 14-NOV-2000; 2000US-0247621P.  
PR 14-NOV-2000; 2000US-0247630P.  
PR 14-NOV-2000; 2000US-0247631P.  
PR 14-NOV-2000; 2000US-0247632P.  
PR 14-NOV-2000; 2000US-0247633P.  
PR 14-NOV-2000; 2000US-0247634P.  
PR 14-NOV-2000; 2000US-0247635P.  
PR 14-NOV-2000; 2000US-0247698P.  
PR 14-NOV-2000; 2000US-0247699P.  
PR 14-NOV-2000; 2000US-0247700P.  
PR 14-NOV-2000; 2000US-0247701P.  
PR 14-NOV-2000; 2000US-0247702P.  
PR 14-NOV-2000; 2000US-0247797P.  
PR 14-NOV-2000; 2000US-0247798P.  
PR 14-NOV-2000; 2000US-0247799P.  
PR 14-NOV-2000; 2000US-0247800P.  
PR 14-NOV-2000; 2000US-0247801P.  
PR 14-NOV-2000; 2000US-0247802P.  
PR 14-NOV-2000; 2000US-0247803P.  
PR 14-NOV-2000; 2000US-0247804P.  
PR 14-NOV-2000; 2000US-0247805P.  
PR 14-NOV-2000; 2000US-0247807P.  
PR 14-NOV-2000; 2000US-0247832P.  
PR 14-NOV-2000; 2000US-0247833P.  
PR 14-NOV-2000; 2000US-0247926P.  
PR 14-NOV-2000; 2000US-0247927P.  
PR 14-NOV-2000; 2000US-0247928P.  
PR 14-NOV-2000; 2000US-0247929P.  
PR 14-NOV-2000; 2000US-0247930P.  
PR 08-MAR-2001; 2001US-0274622P.

XX

PA (PICC/) PICCARIELLO T.

PA (OLON/) OLON L P.

PA (KIRK/) KIRK R J.

XX

PI Piccariello T, Olon LP, Kirk RJ;

XX

DR WPI; 2002-722623/78.

XX

PT Composition useful for protecting active agents from degradation

PT comprises polypeptide covalently attached to active agent.

XX

PS Example 17; Page 19; 34pp; English.

XX

CC The present invention relates to a composition comprising a polypeptide  
CC and an active agent covalently attached to the polypeptide. Also  
CC described is a method for delivery of an active agent to a patient, a  
CC method for protecting an active agent from degradation, and a method for  
CC controlling release of an active agent from a composition. The  
CC polypeptide stabilises the active agent, primarily in the stomach,  
CC through conformational protection and prevents digestion in the stomach.  
CC Delivery of the active agent is controlled, in part, by the kinetics of  
CC unfolding of the carrier peptide to the specific site of action. The  
CC pharmacological effect can be prolonged by delayed release of the active

CC agent. The active agent can be combined to produce a synergistic effect.  
CC The absorption of the active agent in the intestinal tract can be  
CC increased. The present sequence represents a peptide synthesised in the  
CC examples of the present invention

XX

SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 5; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KKKK 8  
| | | |  
Db 1 KKKK 4

# RESULT 53

ABP98787

ID ABP98787 standard; peptide; 11 AA.

XX

AC ABP98787;

XX

DT 25-JUL-2003 (first entry)

XX

DE Peptide #4 for quantitative depletion analysis method.

XX

KW Protein analysis; quantitative depletion analysis; side-chain binding;  
KW pharmacoproteomics; drug target discovery; diagnosis; cancer;  
KW Alzheimer's disease.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "biotinylated N-terminus"

XX

PN WO2003027681-A2.

XX

PD 03-APR-2003.

XX

PF 27-SEP-2002; 2002WO-GB004364.

XX

PR 27-SEP-2001; 2001GB-00023295.

PR 27-SEP-2001; 2001US-0326177P.

XX

PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.

XX

PI Soloviev M, Terrett JA;

XX

DR WPI; 2003-371940/35.

XX

PT Analysis of protein mixtures derived from biological samples useful in  
PT e.g. diagnosis involves contacting a peptide mixture with an amino acid  
PT filtering agent and depleting the mixture followed by identification of  
PT the peptide.

XX

PS Example 1; Page 24; 33pp; English.

XX  
 CC The invention relates to a method of analysing proteins in a mixture by:  
 CC (a) treating the protein mixture to produce a mixture of peptides; (b)  
 CC contacting the peptide mixture with at least one amino acid filtering  
 CC agent that specifically binds the side-chain of an amino acid; (c)  
 CC depleting the peptide mixture that binds to the filtering agent; and (d)  
 CC identifying at least one peptide remaining in the depleted mixture. The  
 CC method is used to analyse a protein mixture derived from a biological  
 CC sample, e.g. for proteomic analysis for determining the physiological or  
 CC biochemical state of a body fluid, tissue, or a cell and for determining  
 CC the protein complement of body fluids or exudates; in pharmacoproteomics;  
 CC for identification of markers of disease; in drug target discovery; in  
 CC diagnosis; in conjunction with therapy; for routine diagnostic  
 CC applications; for quantifying multiple proteins whose expression levels  
 CC best correlate with a physiological or biochemical state; for identifying  
 CC complement of proteins within a sample; and for monitoring a clinical  
 CC study e.g. to evaluate drugs for therapy of a disease e.g. cancer and  
 CC Alzheimer's disease. In an example of the invention 10 synthetic peptides  
 CC (ABP98784-ABP98793) were obtained and used in the method with a  
 CC methionine peptide depletion agent  
 XX  
 SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 6; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EGGK 5  
 ||||  
 Db 8 EGGK 11

RESULT 54  
 AAO27080  
 ID AAO27080 standard; peptide; 11 AA.  
 XX  
 AC AAO27080;  
 XX  
 DT 29-MAY-2003 (first entry)  
 XX  
 DE Fibrinogen E fragment related peptide #5.  
 XX  
 KW Fibrinogen E fragment; vitronectin receptor; modulating angiogenesis;  
 KW vitronectin binding activity.  
 XX  
 OS Unidentified.  
 XX  
 PN WO2003010190-A2.  
 XX  
 PD 06-FEB-2003.  
 XX  
 PF 23-JUL-2002; 2002WO-EP008204.  
 XX  
 PR 23-JUL-2001; 2001GB-00017738.  
 PR 19-FEB-2002; 2002GB-00003882.  
 PR 19-FEB-2002; 2002GB-00003883.  
 XX

PA (NOVS ) NOVARTIS AG.  
PA (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.  
PA (BIOA-) BIOACTA LTD.  
XX  
PI Garcia-Echeverria C, Lewis C, Robinson J;  
XX  
DR WPI; 2003-229636/22.  
XX  
PT Screening for agents that modulate the interaction of the fibrinogen E  
PT fragments or peptide derivatives with a vitronectin receptor, comprises  
PT forming a preparation of a polypeptide, peptide and agent to be tested.  
XX  
PS Claim 12; Page 20; 29pp; English.  
XX  
CC The invention relates to a novel method for screening for the  
CC identification of agents that modulate the interaction of the fibrinogen  
CC E fragment or its peptide derivative with a vitronectin receptor. The  
CC novel method comprises forming a preparation of a polypeptide, peptide  
CC and agent to be tested, and detecting or measuring the effect of the  
CC agent on the interaction of the peptide and polypeptide. The methods are  
CC useful for screening for agents that modulate the interaction of the  
CC fibrinogen E fragment or its peptide derivative with a vitronectin  
CC receptor. The method is also useful for identifying agents with  
CC vitronectin binding activity capable of modulating angiogenesis. This  
CC sequence represents a fibrinogen E fragment peptide relating to the  
CC screening method of the invention. NOTE: The Xaa residues in the peptide  
CC sequence can be any amino acid  
XX  
SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 6; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEGG 4  
||||  
Db 4 AEGG 7

RESULT 55  
AAO27103  
ID AAO27103 standard; peptide; 11 AA.  
XX  
AC AAO27103;  
XX  
DT 29-MAY-2003 (first entry)  
XX  
DE Fibrinogen E fragment variant peptide #3.  
XX  
KW Fibrinogen E fragment; vitronectin receptor; modulating angiogenesis;  
KW vitronectin binding activity; variant.  
XX  
OS Unidentified.  
XX  
PN WO2003010190-A2.  
XX  
PD 06-FEB-2003.

XX  
PF 23-JUL-2002; 2002WO-EP008204.  
XX  
PR 23-JUL-2001; 2001GB-00017738.  
PR 19-FEB-2002; 2002GB-00003882.  
PR 19-FEB-2002; 2002GB-00003883.  
XX  
PA (NOVS ) NOVARTIS AG.  
PA (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.  
PA (BIOA-) BIOACTA LTD.  
XX  
PI Garcia-Echeverria C, Lewis C, Robinson J;  
XX  
DR WPI; 2003-229636/22.  
XX  
PT Screening for agents that modulate the interaction of the fibrinogen E  
PT fragments or peptide derivatives with a vitronectin receptor, comprises  
PT forming a preparation of a polypeptide, peptide and agent to be tested.  
XX  
PS Disclosure; Fig 1; 29pp; English.  
XX  
CC The invention relates to a novel method for screening for the  
CC identification of agents that modulate the interaction of the fibrinogen  
CC E fragment or its peptide derivative with a vitronectin receptor. The  
CC novel method comprises forming a preparation of a polypeptide, peptide  
CC and agent to be tested, and detecting or measuring the effect of the  
CC agent on the interaction of the peptide and polypeptide. The methods are  
CC useful for screening for agents that modulate the interaction of the  
CC fibrinogen E fragment or its peptide derivative with a vitronectin  
CC receptor. The method is also useful for identifying agents with  
CC vitronectin binding activity capable of modulating angiogenesis. This  
CC sequence represents a fibrinogen E fragment variant peptide relating to  
CC the screening method of the invention. NOTE: The Xaa residues in the  
CC peptide sequence can be any amino acid  
XX  
SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 6; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEGG 4  
||||  
Db 4 AEGG 7

RESULT 56  
ADA18540  
ID ADA18540 standard; peptide; 11 AA.  
XX  
AC ADA18540;  
XX  
DT 20-NOV-2003 (first entry)  
XX  
DE Human alpha fibrinogen peptide #2.  
XX  
KW Alpha fibrinogen; human; myocardial infarction; SELDI; mass spectrometry;

KW surfaces enhanced for laser desorption/ionisation.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2002160422-A1.  
 XX  
 PD 31-OCT-2002.  
 XX  
 PF 30-APR-2001; 2001US-00846342.  
 XX  
 PR 30-APR-2001; 2001US-00846342.  
 XX  
 PA (JACK/) JACKOWSKI G.  
 PA (THAT/) THATCHER B.  
 PA (MARS/) MARSHALL J.  
 PA (YANT/) YANTHA J.  
 PA (VREE/) VREES T.  
 XX  
 PI Jackowski G, Thatcher B, Marshall J, Yantha J, Vrees T;  
 XX  
 DR WPI; 2003-219986/21.  
 XX  
 PT Novel biopolymer marker useful in indicating disease state, in particular  
 PT myocardial infarction.  
 XX  
 PS Claim 1; Page 7; 10pp; English.  
 XX  
 CC The invention relates to a biopolymer marker useful in indicating at  
 CC least one particular disease state. This marker is characterised as alpha  
 CC fibrinogen having a molecular weight of 1077 Daltons and is useful for  
 CC indicating a disease state, in particular myocardial infarction. The  
 CC marker sequences are useful as antigens in immunoassays for the detection  
 CC of those individuals suffering from the disease known to be evidenced by  
 CC the marker sequence. The marker provides an efficient diagnostic tool for  
 CC rapidly and accurately diagnosing disease states such as myocardial  
 CC infarction. The marker was detected by the technique of surfaces enhanced  
 CC for laser desorption/ionisation (SELDI) mass spectroscopy. The present  
 CC sequence is the alpha fibrinogen marker peptide.  
 XX  
 SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 6; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEGG 4  
 ||||  
 Db 5 AEGG 8

RESULT 57  
 ADA26448  
 ID ADA26448 standard; peptide; 11 AA.  
 XX  
 AC ADA26448;  
 XX  
 DT 20-NOV-2003 (first entry)

XX  
DE Suitable segment A peptide.  
XX  
KW Molecular marker; separation; characterisation; protein; electrophoresis.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Modified-site 2  
FT /note= "modified with TMR"  
FT Modified-site 3  
FT /note= "modified with TMR"  
FT Modified-site 4  
FT /note= "modified with TMR"  
FT Modified-site 5  
FT /note= "modified with TMR"  
XX  
PN WO2003070967-A2.  
XX  
PD 28-AUG-2003.  
XX  
PF 20-FEB-2003; 2003WO-US004814.  
XX  
PR 20-FEB-2002; 2002US-0357634P.  
XX  
PA (INVI-) INVITROGEN CORP.  
XX  
PI Tadayoni-Rebek M, Amshey JW, Rooney R;  
XX  
DR WPI; 2003-712621/67.  
XX  
PT New marker molecule, useful in electrophoretic diagnosis and genomic  
PT analysis, comprises labeled molecule linked to protein or nucleic acid of  
PT known molecular weight.  
XX  
PS Disclosure; Fig 4; 88pp; English.  
XX  
CC The invention relates to a novel marker molecule with the structure A-L-  
CC B, where A is a labelled molecule, L is a linker or bond, and B is a  
CC protein or nucleic acid. Molecules of the invention are molecular weight  
CC markers for use in electrophoresis, especially for separation or  
CC characterisation of proteins and other molecules. Marker molecules of the  
CC invention are highly homogenous (they have known molecular weight and  
CC isoelectric point and are prepared in a site-specific manner, where only  
CC one coupling reaction can occur, ensuring formation of a single product),  
CC visible, compatible with current separation techniques, especially  
CC electrophoresis, and, when separated, will produce narrow, sharp bands or  
CC spots. They may also be synthesised to include tags for ease of  
CC purification. The current sequence represents a peptide that is used as a  
CC "Segment A" of the marker molecules of the invention. It was created by  
CC solid phase synthesis.  
XX  
SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 6; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KKKK 8  
| | | |  
Db 2 KKKK 5

RESULT 58

ADA23765

ID ADA23765 standard; peptide; 11 AA.

XX

AC ADA23765;

XX

DT 20-NOV-2003 (first entry)

XX

DE Alzheimer's disease-associated protein isoform tryptic peptide #374.

XX

KW human; Alzheimer's disease; vascular dementia; Lewy body dementia;

KW schizophrenia; Parkinson's disease; multiple sclerosis; depression;

KW Alzheimer's disease-associated protein isoform; ADPI.

XX

OS Homo sapiens.

XX

PN US2003064411-A1.

XX

PD 03-APR-2003.

XX

PF 10-DEC-2001; 2001US-00014340.

XX

PR 08-DEC-2000; 2000US-0254431P.

XX

PA (HERA/) HERATH H M A C.

PA (PARE/) PAREKH R B.

PA (ROHL/) ROHLFF C.

XX

PI Herath HMAc, Parekh RB, Rohlff C;

XX

DR WPI; 2003-540784/51.

XX

PT Screening, diagnosis or prognosis of Alzheimer's disease in subject,

PT involves analyzing test sample of brain tissue from subject, and

PT comparing feature in test sample with that of person(s) free from

PT Alzheimer's disease.

XX

PS Disclosure; SEQ ID NO 374; 115pp; English.

XX

CC The invention relates to a method of screening or diagnosing Alzheimer's

CC disease in a subject. The method is useful for screening, diagnosis or

CC prognosis of Alzheimer's disease in a subject for determining the stage

CC of severity of Alzheimer's disease in a subject, for identifying a

CC subject at risk of developing Alzheimer's disease, or for monitoring the

CC effect of therapy administered to a subject having Alzheimer's disease.

CC The method is also useful in treating vascular dementia, Lewy body

CC dementia, schizophrenia, Parkinson's disease, multiple sclerosis or

CC depression. The inventive method identifies sensitive and specific

CC biomarkers for the diagnosis of Alzheimer's disease in living subjects.

CC It provides therapeutic agents for Alzheimer's disease that works

CC quickly, potently, specifically with fewer side effects. The present



CC sequence represents the amino acid sequence of a Alzheimer's disease-  
CC associated protein isoform tryptic peptide.  
XX  
SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 6; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEGG 4  
    ||||  
Db 3 AEGG 6

RESULT 59

ADC35041

ID ADC35041 standard; peptide; 11 AA.

XX

AC ADC35041;

XX

DT 18-DEC-2003 (first entry)

XX

DE RhoA protein transduction domain.

XX

KW protein transduction domain; PTD; cell-penetrating capacity; C-terminus;

KW Ras-like GTPase; Ras-like GTPase inhibition;

KW leukaemic cell migration inhibition; leukaemia; RhoA.

XX

OS Synthetic.

OS Unidentified.

XX

PN WO2003042239-A1.

XX

PD 22-MAY-2003.

XX

PF 11-NOV-2002; 2002WO-NL000722.

XX

PR 12-NOV-2001; 2001EP-00204305.

XX

PA (SANQ-) STICHTING SANQUIN BLOEDVOORZIENING.

XX

PI Ten Klooster JP, Van Hennik PB, Voermans C, Hordijk PL;

XX

DR WPI; 2003-568944/53.

XX

PT New protein transduction domain peptides having cell-penetrating

PT capacity, are useful for inhibiting cellular functions mediated by the

PT Ras-like GTPase in eukaryotic cells, and for inhibiting leukemic cell

PT migration.

XX

PS Claim 9; Page 29; 46pp; English.

XX

CC The invention comprises amino acid sequences corresponding to a protein

CC transduction domain (PTD) which has a cell-penetrating capacity and an

CC amino acid sequence corresponding to a variable part of the C-terminus of

CC a Ras-like GTPase having Ras-like GTPase signalling capacity. The

CC peptides of the invention are useful for inhibiting cellular functions

CC mediated by the Ras-like GTPase in eukaryotic cells - particularly  
CC mammalian cells, and for inhibiting leukaemic cell migration. The present  
CC amino acid sequence represents a RhoA protein transduction domain of the  
CC invention.  
XX  
SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 7; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GKKK 7  
||||  
Db 6 GKKK 9

RESULT 60

ADC35004

ID ADC35004 standard; peptide; 11 AA.

XX

AC ADC35004;

XX

DT 18-DEC-2003 (first entry)

XX

DE Rho-like protein C-terminal peptide #1.

XX

KW protein transduction domain; PTD; cell-penetrating capacity; C-terminus;

KW Ras-like GTPase; Ras-like GTPase inhibition;

KW leukaemic cell migration inhibition; leukaemia; Rho-like protein.

XX

OS Unidentified.

XX

PN WO2003042239-A1.

XX

PD 22-MAY-2003.

XX

PF 11-NOV-2002; 2002WO-NL000722.

XX

PR 12-NOV-2001; 2001EP-00204305.

XX

PA (SANQ-) STICHTING SANQUIN BLOEDVOORZIENING.

XX

PI Ten Klooster JP, Van Hennik PB, Voermans C, Hordijk PL;

XX

DR WPI; 2003-568944/53.

XX

PT New protein transduction domain peptides having cell-penetrating  
PT capacity, are useful for inhibiting cellular functions mediated by the  
PT Ras-like GTPase in eukaryotic cells, and for inhibiting leukemic cell  
PT migration.

XX

PS Disclosure; Page 14; 46pp; English.

XX

CC The invention comprises amino acid sequences corresponding to a protein  
CC transduction domain (PTD) which has a cell-penetrating capacity and an  
CC amino acid sequence corresponding to a variable part of the C-terminus of  
CC a Ras-like GTPase having Ras-like GTPase signalling capacity. The

CC peptides of the invention are useful for inhibiting cellular functions  
CC mediated by the Ras-like GTPase in eukaryotic cells - particularly  
CC mammalian cells, and for inhibiting leukaemic cell migration. The present  
CC amino acid sequence represents a C-terminal sequence from a Rho-like  
CC protein.

XX

SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 7; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GKKK 7

||||

Db 6 GKKK 9

#### RESULT 61

ADE10861

ID ADE10861 standard; peptide; 11 AA.

XX

AC ADE10861;

XX

DT 29-JAN-2004 (first entry)

XX

DE Chimeric hepatitis B virus related B-cell epitope seqid 95.

XX

KW hepatotropic; virucide; antiinflammatory; chronic hepatitis; vaccine;

KW recombinant hepatitis B core chimeric protein; HBc chimeric protein;

KW hepatitis B infection; T-cel stimulator; B-cell epitope.

XX

OS Neisseria meningitidis.

XX

PN US2003198645-A1.

XX

PD 23-OCT-2003.

XX

PF 21-FEB-2003; 2003US-00372076.

XX

PR 21-FEB-2002; 2002US-00080299.

PR 21-FEB-2002; 2002US-00082014.

XX

PA (PAGE/) PAGE M.

PA (FRIE/) FRIEDE M.

XX

PI Page M, Friede M;

XX

DR WPI; 2003-852775/79.

XX

PT Treating chronic hepatitis B infection by administering a T cell-  
PT stimulating vaccine containing immunogenic particles having recombinant  
PT carboxy-terminal truncated hepatitis B core (HBc) chimeric protein  
PT molecules.

XX

PS Disclosure; SEQ ID NO 95; 11lpp; English.

XX

CC The invention describes a method of treating chronic hepatitis comprising

CC administering to a patient a T cell-stimulating amount of a vaccine  
 CC comprising immunogenic particles dissolved or dispersed in a diluent,  
 CC where the immunogenic particles consists of recombinant hepatitis B core  
 CC (HBc) chimeric protein molecules, and maintaining the patient to induce T  
 CC cells activated against HBc. The methods and compositions of the present  
 CC invention are useful for treating chronic hepatitis B infection. This is  
 CC the amino acid sequence of a chimeric hepatitis B virus related B-cell  
 CC epitope useful for expression within the HBV chimera at the N-terminus,  
 CC within the immunogenic loop and/or at the C-terminus.  
 XX  
 SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 7; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 KKKM 9  
 ||||  
 Db 5 KKKM 8

# RESULT 62

AAR24537

ID AAR24537 standard; protein; 11 AA.

XX

AC AAR24537;

XX

DT 25-MAR-2003 (revised)

DT 04-JAN-1992 (first entry)

XX

DE Sequence of a cancer cell infiltration inhibiting peptide.

XX

KW Cancer cell infiltration inhibiting peptide; metastasis therapy.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Misc-difference 7. .11

FT /note= "1-5 AAs may optionally be omitted, sequentially,  
 FT from C-terminal"

XX

PN W09209627-A1.

XX

PD 11-JUN-1992.

XX

PF 29-NOV-1991; 91WO-JP001648.

XX

PR 30-NOV-1990; 90JP-00330612.

PR 05-FEB-1991; 91JP-00035260.

PR 29-MAR-1991; 91JP-00091305.

PR 29-MAR-1991; 91JP-00091306.

XX

PA (ASAG ) ASAHI GLASS CO LTD.

XX

PI Isoai A, Hama Y, Kumagai H;

XX

DR WPI; 1992-217020/26.

XX  
PT New cancer cell infiltration inhibiting peptide - comprises 5-20  
PT aminoacid residues and a biopolymer for treating cancer metastasis.  
XX  
PS Claim 2; Page 19; 29pp; Japanese.  
XX  
CC The peptides of the invention may be used as cancer metastasis  
CC inhibitors. They possess human cancer cell infiltration inhibitor  
CC activity. They may be bound to a non-toxic organic high mol. wt.  
CC substance such as a protein, chondroitin sulphate or hyaluronic acid.  
CC (Updated on 25-MAR-2003 to correct PN field.)  
XX  
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.3e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEG 3  
|||  
Db 4 AEG 6

# RESULT 63

AAR24543

ID AAR24543 standard; protein; 11 AA.

XX

AC AAR24543;

XX

DT 25-MAR-2003 (revised)

DT 04-JAN-1992 (first entry)

XX

DE Sequence of a cancer cell infiltration inhibiting peptide.

XX

KW Cancer cell infiltration inhibiting peptide; metastasis therapy.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Misc-difference 7. .11

FT /note= "1-5 AAs may optionally be omitted, sequentially,  
FT from C-terminal"

XX

PN W09209627-A1.

XX

PD 11-JUN-1992.

XX

PF 29-NOV-1991; 91WO-JP001648.

XX

PR 30-NOV-1990; 90JP-00330612.

PR 05-FEB-1991; 91JP-00035260.

PR 29-MAR-1991; 91JP-00091305.

PR 29-MAR-1991; 91JP-00091306.

XX

PA (ASAG ) ASAHI GLASS CO LTD.

XX

PI Isoai A, Hama Y, Kumagai H;

XX  
 DR WPI; 1992-217020/26.  
 XX  
 PT New cancer cell infiltration inhibiting peptide - comprises 5-20  
 PT aminoacid residues and a biopolymer for treating cancer metastasis.  
 XX  
 PS Claim 2; Page 19; 29pp; Japanese.  
 XX  
 CC The peptides of the invention may be used as cancer metastasis  
 CC inhibitors. They possess human cancer cell infiltration inhibitor  
 CC activity. They may be bound to a non-toxic organic high mol. wt.  
 CC substance such as a protein, chondroitin sulphate or hyaluronic acid.  
 CC (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEG 3  
 |||  
 Db 4 AEG 6

# RESULT 64

AAR24539

ID AAR24539 standard; protein; 11 AA.

XX

AC AAR24539;

XX

DT 25-MAR-2003 (revised)

DT 04-JAN-1992 (first entry)

XX

DE Sequence of a cancer cell infiltration inhibiting peptide.

XX

KW Cancer cell infiltration inhibiting peptide; metastasis therapy.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Misc-difference 7. .11

FT /note= "1-5 AAs may optionally be omitted, sequentially,  
 FT from C-terminal"

XX

PN WO9209627-A1.

XX

PD 11-JUN-1992.

XX

PF 29-NOV-1991; 91WO-JP001648.

XX

PR 30-NOV-1990; 90JP-00330612.

PR 05-FEB-1991; 91JP-00035260.

PR 29-MAR-1991; 91JP-00091305.

PR 29-MAR-1991; 91JP-00091306.

XX

PA (ASAG ) ASAHI GLASS CO LTD.

XX  
 PI Isoai A, Hama Y, Kumagai H;  
 XX  
 DR WPI; 1992-217020/26.  
 XX  
 PT New cancer cell infiltration inhibiting peptide - comprises 5-20  
 PT aminoacid residues and a biopolymer for treating cancer metastasis.  
 XX  
 PS Claim 2; Page 19; 29pp; Japanese.  
 XX  
 CC The peptides of the invention may be used as cancer metastasis  
 CC inhibitors. They possess human cancer cell infiltration inhibitor  
 CC activity. They may be bound to a non-toxic organic high mol. wt.  
 CC substance such as a protein, chondroitin sulphate or hyaluronic acid.  
 CC (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEG 3  
 |||  
 Db 4 AEG 6

# RESULT 65

AAR24536

ID AAR24536 standard; protein; 11 AA.

XX

AC AAR24536;

XX

DT 25-MAR-2003 (revised)

DT 04-JAN-1992 (first entry)

XX

DE Sequence of a cancer cell infiltration inhibiting peptide.

XX

KW Cancer cell infiltration inhibiting peptide; metastasis therapy.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Misc-difference 7. .11

FT /note= "1-5 AAs may optionally be omitted, sequentially,  
 FT from C-terminal"

XX

PN WO9209627-A1.

XX

PD 11-JUN-1992.

XX

PF 29-NOV-1991; 91WO-JP001648.

XX

PR 30-NOV-1990; 90JP-00330612.

PR 05-FEB-1991; 91JP-00035260.

PR 29-MAR-1991; 91JP-00091305.

PR 29-MAR-1991; 91JP-00091306.

XX  
 PA (ASAG ) ASAHI GLASS CO LTD.  
 XX  
 PI Isoai A, Hama Y, Kumagai H;  
 XX  
 DR WPI; 1992-217020/26.  
 XX  
 PT New cancer cell infiltration inhibiting peptide - comprises 5-20  
 PT aminoacid residues and a biopolymer for treating cancer metastasis.  
 XX  
 PS Claim 2; Page 19; 29pp; Japanese.  
 XX  
 CC The peptides of the invention may be used as cancer metastasis  
 CC inhibitors. They possess human cancer cell infiltration inhibitor  
 CC activity. They may be bound to a non-toxic organic high mol. wt.  
 CC substance such as a protein, chondroitin sulphate or hyaluronic acid.  
 CC (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 11 AA;  
  
 Query Match 27.3%; Score 3; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 Qy 1 AEG 3  
 |||  
 Db 4 AEG 6

RESULT 66

AAR27765

ID AAR27765 standard; peptide; 11 AA.  
 XX  
 AC AAR27765;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 03-MAR-1993 (first entry)  
 XX  
 DE BSA-binding disulphide-constrained micropeptide #1.  
 XX  
 KW Potential binding domain; TN2 phage library; bovine serum albumen.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Disulfide-bond 4. .9  
 XX  
 PN WO9215677-A1.  
 XX  
 PD 17-SEP-1992.  
 XX  
 PF 27-FEB-1992; 92WO-US001456.  
 XX  
 PR 01-MAR-1991; 91US-00664989.  
 XX  
 PA (PROT-) PROTEIN ENG CORP.  
 XX



PI Ladner RC, Roberts BL, Ley AC, Kent RB;  
 XX  
 DR WPI; 1992-331723/40.  
 XX  
 PT Developing binding proteins for target material - using library  
 PT displaying chimeric micro-proteins having intra-chain covalent crosslink.  
 XX  
 PS Example 1; Page 123; 151pp; English.  
 XX  
 CC DNA coding for a family of microproteins containing a cystine moiety with  
 CC a disulphide bridge span of 4 amino acids was fused to the gene III of  
 CC M13. The fusion proteins were displayed on the phage surface. The library  
 CC was screened for streptavidin binding micropeptides; the phage were bound  
 CC to bovine serum albumen-coated wells and bound phage were eluted and used  
 CC to infect bacteria. New phage stock was harvested for two further  
 CC enhancement cycles, after which some of the individual phage were  
 CC sequenced and tested. Micropeptide #1 is one of the peptide sequences  
 CC which bound to BSA; there was no consensus motif between the cysteine  
 CC residues of the 8 micropeptides isolated by this procedure. See also  
 CC AAR27766-R27772. (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EGG 4  
 |||  
 Db 1 EGG 3

# RESULT 67

AAR27771

ID AAR27771 standard; peptide; 11 AA.

XX

AC AAR27771;

XX

DT 25-MAR-2003 (revised)

DT 03-MAR-1993 (first entry)

XX

DE BSA-binding disulphide-constrained micropeptide #7.

XX

KW Potential binding domain; TN2 phage library; bovine serum albumen.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Disulfide-bond 4. .9

XX

PN WO9215677-A1.

XX

PD 17-SEP-1992.

XX

PF 27-FEB-1992; 92WO-US001456.

XX

PR 01-MAR-1991; 91US-00664989.

XX  
 PA (PROT-) PROTEIN ENG CORP.  
 XX  
 PI Ladner RC, Roberts BL, Ley AC, Kent RB;  
 XX  
 DR WPI; 1992-331723/40.  
 XX  
 PT Developing binding proteins for target material - using library  
 PT displaying chimeric micro-proteins having intra-chain covalent crosslink.  
 XX  
 PS Example 1; Page 123; 15lpp; English.  
 XX  
 CC DNA coding for a family of microproteins containing a cystine moiety with  
 CC a disulphide bridge span of 4 amino acids was fused to the gene III of  
 CC M13. The fusion proteins were displayed on the phage surface. The library  
 CC was screened for streptavidin binding micropeptides; the phage were bound  
 CC to bovine serum albumen-coated wells and bound phage were eluted and used  
 CC to infect bacteria. New phage stock was harvested for two further  
 CC enhancement cycles, after which some of the individual phage were  
 CC sequenced and tested. Micropeptide #7 is one of the peptide sequences  
 CC which bound to BSA; there was no consensus motif between the cysteine  
 CC residues of the 8 micropeptides isolated by this procedure. See also  
 CC AAR27765-R27772. (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EGG 4  
 |||  
 Db 1 EGG 3

# RESULT 68

AAR41837

ID AAR41837 standard; peptide; 11 AA.

XX

AC AAR41837;

XX

DT 25-MAR-2003 (revised)

DT 23-MAR-1994 (first entry)

XX

DE Phospholipase C inhibitory peptide #12.

XX

KW PLC; inhibitor; anti-bacterial; anti-microbial; phospholipase.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "N-Coumaryl-L-Leu"

FT Modified-site 11

FT /note= "amidated"

XX

PN W09318062-A1.

XX  
PD 16-SEP-1993.  
XX  
PF 11-MAR-1993; 93WO-JP000299.  
XX  
PR 11-MAR-1992; 92JP-00052394.  
XX  
PA (KYOW ) KYOWA HAKKO KOGYO CO LTD.  
XX  
PI Saito H, Ishikawa G, Yamasaki M, Honma Y;  
XX  
DR WPI; 1993-303402/38.  
XX  
PT Mutant peptide having phospholipase C inhibiting activity - with  
PT specified aminoacid sequence or modified sequence.  
XX  
PS Claim 4; Page 35; 53pp; Japanese.  
XX  
CC Phospholipase C inhibitor peptides are derived from sequence AAR41826 by  
CC deletion, substitution or addition of at least 1 amino acid (see AAR41827  
CC -R41833 for specifically claimed mutant peptides). The amino acids in the  
CC inhibitory peptides, especially the N- and C- terminal residues can also  
CC be modified (see AAR41834-R41853 for specific examples). The PLC  
CC inhibitors also inhibit cell proliferation and have good antibacterial  
CC properties. (Updated on 25-MAR-2003 to correct PN field.)  
XX  
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.3e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KMR 10  
|||  
Db 4 KMR 6

# RESULT 69

AAR41846

ID AAR41846 standard; peptide; 11 AA.

XX

AC AAR41846;

XX

DT 25-MAR-2003 (revised)

DT 23-MAR-1994 (first entry)

XX

DE Phospholipase C inhibitory peptide #21.

XX

KW PLC; inhibitor; anti-bacterial; anti-microbial; phospholipase.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "N-(n-Caprylyl)-L-Leu"

FT Modified-site 11

FT /note= "amidated"

XX  
 PN WO9318062-A1.  
 XX  
 PD 16-SEP-1993.  
 XX  
 PF 11-MAR-1993; 93WO-JP000299.  
 XX  
 PR 11-MAR-1992; 92JP-00052394.  
 XX  
 PA (KYOW ) KYOWA HAKKO KOGYO CO LTD.  
 XX  
 PI Saito H, Ishikawa G, Yamasaki M, Honma Y;  
 XX  
 DR WPI; 1993-303402/38.  
 XX  
 PT Mutant peptide having phospholipase C inhibiting activity - with  
 PT specified aminoacid sequence or modified sequence.  
 XX  
 PS Claim 4; Page 41; 53pp; Japanese.  
 XX  
 CC Phospholipase C inhibitor peptides are derived from sequence AAR41826 by  
 CC deletion, substitution or addition of at least 1 amino acid (see AAR41827  
 CC -R41833 for specifically claimed mutant peptides). The amino acids in the  
 CC inhibitory peptides, especially the N- and C- terminal residues can also  
 CC be modified (see AAR41834-R41853 for specific examples). The PLC  
 CC inhibitors also inhibit cell proliferation and have good antibacterial  
 CC properties. (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KMR 10  
 |||  
 Db 4 KMR 6

# RESULT 70

AAR41844

ID AAR41844 standard; peptide; 11 AA.

XX

AC AAR41844;

XX

DT 25-MAR-2003 (revised)

DT 23-MAR-1994 (first entry)

XX

DE Phospholipase C inhibitory peptide #19.

XX

KW PLC; inhibitor; anti-bacterial; anti-microbial; phospholipase.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "N-Isobutyryl-L-Leu"

FT Modified-site 11  
 FT /note= "amidated"  
 XX  
 PN WO9318062-A1.  
 XX  
 PD 16-SEP-1993.  
 XX  
 PF 11-MAR-1993; 93WO-JP000299.  
 XX  
 PR 11-MAR-1992; 92JP-00052394.  
 XX  
 PA (KYOW ) KYOWA HAKKO KOGYO CO LTD.  
 XX  
 PI Saito H, Ishikawa G, Yamasaki M, Honma Y;  
 XX  
 DR WPI; 1993-303402/38.  
 XX  
 PT Mutant peptide having phospholipase C inhibiting activity - with  
 PT specified aminoacid sequence or modified sequence.  
 XX  
 PS Claim 4; Page 40; 53pp; Japanese.  
 XX  
 CC Phospholipase C inhibitor peptides are derived from sequence AAR41826 by  
 CC deletion, substitution or addition of at least 1 amino acid (see AAR41827  
 CC -R41833 for specifically claimed mutant peptides). The amino acids in the  
 CC inhibitory peptides, especially the N- and C- terminal residues can also  
 CC be modified (see AAR41834-R41853 for specific examples). The PLC  
 CC inhibitors also inhibit cell proliferation and have good antibacterial  
 CC properties. (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KMR 10  
 |||  
 Db 4 KMR 6

# RESULT 71

AAR41830

ID AAR41830 standard; peptide; 11 AA.

XX

AC AAR41830;

XX

DT 25-MAR-2003 (revised)

DT 23-MAR-1994 (first entry)

XX

DE Phospholipase C inhibitory peptide #5.

XX

KW PLC; inhibitor; anti-bacterial; anti-microbial; phospholipase.

XX

OS Synthetic.

XX

PN WO9318062-A1.

XX  
PD 16-SEP-1993.  
XX  
PF 11-MAR-1993; 93WO-JP000299.  
XX  
PR 11-MAR-1992; 92JP-00052394.  
XX  
PA (KYOW ) KYOWA HAKKO KOGYO CO LTD.  
XX  
PI Saito H, Ishikawa G, Yamasaki M, Honma Y;  
XX  
DR WPI; 1993-303402/38.  
XX  
PT Mutant peptide having phospholipase C inhibiting activity - with  
PT specified aminoacid sequence or modified sequence.  
XX  
PS Claim 2; Page 32; 53pp; Japanese.  
XX  
CC Phospholipase C inhibitor peptides are derived from sequence AAR41826 by  
CC deletion, substitution or addition of at least 1 amino acid (see AAR41827  
CC -R41833 for specifically claimed mutant peptides). The amino acids in the  
CC inhibitory peptides, especially the N- and C- terminal residues can also  
CC be modified (see AAR41834-R41853 for specific examples). The PLC  
CC inhibitors also inhibit cell proliferation and have good antibacterial  
CC properties. (Updated on 25-MAR-2003 to correct PN field.)  
XX  
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.3e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KMR 10  
|||  
Db 4 KMR 6

# RESULT 72

AAR41843

ID AAR41843 standard; peptide; 11 AA.

XX

AC AAR41843;

XX

DT 25-MAR-2003 (revised)

DT 23-MAR-1994 (first entry)

XX

DE Phospholipase C inhibitory peptide #18.

XX

KW PLC; inhibitor; anti-bacterial; anti-microbial; phospholipase.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "N-Propionyl-L-Leu"

FT Modified-site 11

FT /note= "amidated"

XX  
 PN WO9318062-A1.  
 XX  
 PD 16-SEP-1993.  
 XX  
 PF 11-MAR-1993; 93WO-JP000299.  
 XX  
 PR 11-MAR-1992; 92JP-00052394.  
 XX  
 PA (KYOW ) KYOWA HAKKO KOGYO CO LTD.  
 XX  
 PI Saito H, Ishikawa G, Yamasaki M, Honma Y;  
 XX  
 DR WPI; 1993-303402/38.  
 XX  
 PT Mutant peptide having phospholipase C inhibiting activity - with  
 PT specified aminoacid sequence or modified sequence.  
 XX  
 PS Claim 4; Page 39; 53pp; Japanese.  
 XX  
 CC Phospholipase C inhibitor peptides are derived from sequence AAR41826 by  
 CC deletion, substitution or addition of at least 1 amino acid (see AAR41827  
 CC -R41833 for specifically claimed mutant peptides). The amino acids in the  
 CC inhibitory peptides, especially the N- and C- terminal residues can also  
 CC be modified (see AAR41834-R41853 for specific examples). The PLC  
 CC inhibitors also inhibit cell proliferation and have good antibacterial  
 CC properties. (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KMR 10  
 |||  
 Db 4 KMR 6

# RESULT 73

AAR41842

ID AAR41842 standard; peptide; 11 AA.

XX

AC AAR41842;

XX

DT 25-MAR-2003 (revised)

DT 23-MAR-1994 (first entry)

XX

DE Phospholipase C inhibitory peptide #17.

XX

KW PLC; inhibitor; anti-bacterial; anti-microbial; phospholipase.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "N-Cyclopentylacetyl-L-Leu"

FT Modified-site 11  
 FT /note= "amidated"  
 XX  
 PN WO9318062-A1.  
 XX  
 PD 16-SEP-1993.  
 XX  
 PF 11-MAR-1993; 93WO-JP000299.  
 XX  
 PR 11-MAR-1992; 92JP-00052394.  
 XX  
 PA (KYOW ) KYOWA HAKKO KOGYO CO LTD.  
 XX  
 PI Saito H, Ishikawa G, Yamasaki M, Honma Y;  
 XX  
 DR WPI; 1993-303402/38.  
 XX  
 PT Mutant peptide having phospholipase C inhibiting activity - with  
 PT specified aminoacid sequence or modified sequence.  
 XX  
 PS Claim 4; Page 39; 53pp; Japanese.  
 XX  
 CC Phospholipase C inhibitor peptides are derived from sequence AAR41826 by  
 CC deletion, substitution or addition of at least 1 amino acid (see AAR41827  
 CC -R41833 for specifically claimed mutant peptides). The amino acids in the  
 CC inhibitory peptides, especially the N- and C- terminal residues can also  
 CC be modified (see AAR41834-R41853 for specific examples). The PLC  
 CC inhibitors also inhibit cell proliferation and have good antibacterial  
 CC properties. (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KMR 10  
 |||  
 Db 4 KMR 6

#### RESULT 74

AAR41853

ID AAR41853 standard; peptide; 11 AA.

XX

AC AAR41853;

XX

DT 25-MAR-2003 (revised)

DT 23-MAR-1994 (first entry)

XX

DE Phospholipase C inhibitory peptide #28.

XX

KW PLC; inhibitor; anti-bacterial; anti-microbial; phospholipase.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers



FT Modified-site 1  
 FT /note= "N-(n-Nonanoyl)-L-Leu"  
 FT Modified-site 11  
 FT /note= "amidated"  
 XX  
 PN WO9318062-A1.  
 XX  
 PD 16-SEP-1993.  
 XX  
 PF 11-MAR-1993; 93WO-JP000299.  
 XX  
 PR 11-MAR-1992; 92JP-00052394.  
 XX  
 PA (KYOW ) KYOWA HAKKO KOGYO CO LTD.  
 XX  
 PI Saito H, Ishikawa G, Yamasaki M, Honma Y;  
 XX  
 DR WPI; 1993-303402/38.  
 XX  
 PT Mutant peptide having phospholipase C inhibiting activity - with  
 PT specified aminoacid sequence or modified sequence.  
 XX  
 PS Claim 4; Page 46; 53pp; Japanese.  
 XX  
 CC Phospholipase C inhibitor peptides are derived from sequence AAR41826 by  
 CC deletion, substitution or addition of at least 1 amino acid (see AAR41827  
 CC -R41833 for specifically claimed mutant peptides). The amino acids in the  
 CC inhibitory peptides, especially the N- and C- terminal residues can also  
 CC be modified (see AAR41834-R41853 for specific examples). The PLC  
 CC inhibitors also inhibit cell proliferation and have good antibacterial  
 CC properties. (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KMR 10  
 |||  
 Db 4 KMR 6

# RESULT 75

AAR41845

ID AAR41845 standard; peptide; 11 AA.

XX

AC AAR41845;

XX

DT 25-MAR-2003 (revised)

DT 23-MAR-1994 (first entry)

XX

DE Phospholipase C inhibitory peptide #20.

XX

KW PLC; inhibitor; anti-bacterial; anti-microbial; phospholipase.

XX

OS Synthetic.

XX  
 FH Key Location/Qualifiers  
 FT Modified-site 1  
 FT /note= "N-(2-Ethyl-n-butyryl)-L-Leu"  
 FT Modified-site 11  
 FT /note= "amidated"  
 XX  
 PN WO9318062-A1.  
 XX  
 PD 16-SEP-1993.  
 XX  
 PF 11-MAR-1993; 93WO-JP000299.  
 XX  
 PR 11-MAR-1992; 92JP-00052394.  
 XX  
 PA (KYOW ) KYOWA HAKKO KOGYO CO LTD.  
 XX  
 PI Saito H, Ishikawa G, Yamasaki M, Honma Y;  
 XX  
 DR WPI; 1993-303402/38.  
 XX  
 PT Mutant peptide having phospholipase C inhibiting activity - with  
 PT specified aminoacid sequence or modified sequence.  
 XX  
 PS Claim 4; Page 41; 53pp; Japanese.  
 XX  
 CC Phospholipase C inhibitor peptides are derived from sequence AAR41826 by  
 CC deletion, substitution or addition of at least 1 amino acid (see AAR41827  
 CC -R41833 for specifically claimed mutant peptides). The amino acids in the  
 CC inhibitory peptides, especially the N- and C- terminal residues can also  
 CC be modified (see AAR41834-R41853 for specific examples). The PLC  
 CC inhibitors also inhibit cell proliferation and have good antibacterial  
 CC properties. (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KMR 10  
 |||  
 Db 4 KMR 6

Search completed: April 8, 2004, 15:40:08  
 Job time : 44.3077 secs

OM protein - protein search, using sw model

Run on: April 8, 2004, 15:30:08 ; Search time 11.3077 Seconds  
 (without alignments)  
 50.221 Million cell updates/sec

Title: US-09-787-443A-19  
 Perfect score: 11  
 Sequence: 1 AEGGKKKKMRA 11

Scoring table: OLIGO  
 Gapop 60.0 , Gapext 60.0

Searched: 389414 seqs, 51625971 residues

Word size : 0

Total number of hits satisfying chosen parameters: 8542

Minimum DB seq length: 11  
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Post-processing: Listing first 100 summaries

Database : Issued Patents\_AA:\*  
 1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep:\*  
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 4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep:\*  
 5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep:\*  
 6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	%		Query Match Length DB	ID	Description
	Score				
1	6	54.5	11 3	US-08-105-904B-9	Sequence 9, Appli
2	6	54.5	11 3	US-08-105-904B-21	Sequence 21, Appl
3	6	54.5	11 3	US-08-114-877A-9	Sequence 9, Appli
4	6	54.5	11 3	US-08-114-877A-14	Sequence 14, Appl
5	4	36.4	11 1	US-07-694-983-15	Sequence 15, Appl
6	4	36.4	11 3	US-08-592-500-39	Sequence 39, Appl
7	4	36.4	11 3	US-08-970-833-8	Sequence 8, Appli
8	4	36.4	11 3	US-08-195-006-39	Sequence 39, Appl
9	4	36.4	11 4	US-08-584-043A-5	Sequence 5, Appli
10	4	36.4	11 4	US-08-584-043A-43	Sequence 43, Appl
11	4	36.4	11 4	US-08-584-043A-99	Sequence 99, Appl

12	4	36.4	11	4	US-09-082-358B-11	Sequence 11, Appl
13	4	36.4	11	4	US-09-579-664B-33	Sequence 33, Appl
14	4	36.4	11	5	PCT-US94-07644A-39	Sequence 39, Appl
15	4	36.4	11	6	5219739-40	Patent No. 5219739
16	3	27.3	11	1	US-07-664-989B-17	Sequence 17, Appl
17	3	27.3	11	1	US-07-718-274A-31	Sequence 31, Appl
18	3	27.3	11	1	US-08-029-333-4	Sequence 4, Appli
19	3	27.3	11	1	US-08-029-333-30	Sequence 30, Appl
20	3	27.3	11	1	US-08-029-333-32	Sequence 32, Appl
21	3	27.3	11	1	US-08-029-333-33	Sequence 33, Appl
22	3	27.3	11	1	US-08-029-333-46	Sequence 46, Appl
23	3	27.3	11	1	US-08-149-106-31	Sequence 31, Appl
24	3	27.3	11	1	US-07-603-675-8	Sequence 8, Appli
25	3	27.3	11	1	US-08-127-278-6	Sequence 6, Appli
26	3	27.3	11	1	US-08-298-021-31	Sequence 31, Appl
27	3	27.3	11	1	US-08-211-942-18	Sequence 18, Appl
28	3	27.3	11	1	US-08-178-570-75	Sequence 75, Appl
29	3	27.3	11	1	US-08-146-152-5	Sequence 5, Appli
30	3	27.3	11	1	US-08-146-152-11	Sequence 11, Appl
31	3	27.3	11	1	US-08-146-152-12	Sequence 12, Appl
32	3	27.3	11	1	US-08-146-152-13	Sequence 13, Appl
33	3	27.3	11	1	US-08-146-152-14	Sequence 14, Appl
34	3	27.3	11	1	US-08-146-152-15	Sequence 15, Appl
35	3	27.3	11	1	US-08-146-152-16	Sequence 16, Appl
36	3	27.3	11	1	US-08-146-152-17	Sequence 17, Appl
37	3	27.3	11	1	US-08-146-152-18	Sequence 18, Appl
38	3	27.3	11	1	US-08-146-152-19	Sequence 19, Appl
39	3	27.3	11	1	US-08-146-152-20	Sequence 20, Appl
40	3	27.3	11	1	US-08-146-152-21	Sequence 21, Appl
41	3	27.3	11	1	US-08-146-152-22	Sequence 22, Appl
42	3	27.3	11	1	US-08-146-152-23	Sequence 23, Appl
43	3	27.3	11	1	US-08-146-152-24	Sequence 24, Appl
44	3	27.3	11	1	US-08-146-152-25	Sequence 25, Appl
45	3	27.3	11	1	US-08-146-152-26	Sequence 26, Appl
46	3	27.3	11	1	US-08-146-152-27	Sequence 27, Appl
47	3	27.3	11	1	US-08-146-152-28	Sequence 28, Appl
48	3	27.3	11	1	US-08-555-860-6	Sequence 6, Appli
49	3	27.3	11	1	US-08-347-000-4	Sequence 4, Appli
50	3	27.3	11	1	US-08-465-325-128	Sequence 128, App
51	3	27.3	11	1	US-08-416-035-8	Sequence 8, Appli
52	3	27.3	11	1	US-08-082-269D-2	Sequence 2, Appli
53	3	27.3	11	1	US-08-408-604A-50	Sequence 50, Appl
54	3	27.3	11	1	US-08-511-662-5	Sequence 5, Appli
55	3	27.3	11	2	US-08-807-030-42	Sequence 42, Appl
56	3	27.3	11	2	US-08-478-386A-59	Sequence 59, Appl
57	3	27.3	11	2	US-08-292-597-59	Sequence 59, Appl
58	3	27.3	11	2	US-08-719-758-3	Sequence 3, Appli
59	3	27.3	11	2	US-08-244-496-29	Sequence 29, Appl
60	3	27.3	11	2	US-08-701-124-19	Sequence 19, Appl
61	3	27.3	11	2	US-08-621-803-206	Sequence 206, App
62	3	27.3	11	2	US-08-621-259A-181	Sequence 181, App
63	3	27.3	11	2	US-08-388-653-59	Sequence 59, Appl
64	3	27.3	11	2	US-08-473-985-59	Sequence 59, Appl
65	3	27.3	11	2	US-08-938-367-1	Sequence 1, Appli
66	3	27.3	11	2	US-08-053-451B-159	Sequence 159, App
67	3	27.3	11	2	US-08-483-898-59	Sequence 59, Appl
68	3	27.3	11	3	US-08-369-643-75	Sequence 75, Appl

69	3	27.3	11	3	US-08-750-419A-29	Sequence 29, Appl
70	3	27.3	11	3	US-09-087-716-59	Sequence 59, Appl
71	3	27.3	11	3	US-09-015-003-5	Sequence 5, Appli
72	3	27.3	11	3	US-09-157-753-59	Sequence 59, Appl
73	3	27.3	11	3	US-09-157-230-59	Sequence 59, Appl
74	3	27.3	11	3	US-09-087-811-59	Sequence 59, Appl
75	3	27.3	11	3	US-09-130-225-19	Sequence 19, Appl
76	3	27.3	11	3	US-09-156-855-59	Sequence 59, Appl
77	3	27.3	11	3	US-08-893-749-17	Sequence 17, Appl
78	3	27.3	11	3	US-08-915-498B-22	Sequence 22, Appl
79	3	27.3	11	3	US-09-068-738A-15	Sequence 15, Appl
80	3	27.3	11	3	US-09-158-010-59	Sequence 59, Appl
81	3	27.3	11	3	US-09-087-647-59	Sequence 59, Appl
82	3	27.3	11	3	US-08-974-549A-98	Sequence 98, Appl
83	3	27.3	11	3	US-08-652-877-59	Sequence 59, Appl
84	3	27.3	11	3	US-09-130-242-10	Sequence 10, Appl
85	3	27.3	11	3	US-09-206-059-6	Sequence 6, Appli
86	3	27.3	11	3	US-09-206-059-19	Sequence 19, Appl
87	3	27.3	11	3	US-09-119-827-3	Sequence 3, Appli
88	3	27.3	11	3	US-08-995-172-16	Sequence 16, Appl
89	3	27.3	11	3	US-09-307-265A-14	Sequence 14, Appl
90	3	27.3	11	3	US-09-177-249-253	Sequence 253, App
91	3	27.3	11	3	US-08-476-515A-59	Sequence 59, Appl
92	3	27.3	11	3	US-08-865-468-8	Sequence 8, Appli
93	3	27.3	11	3	US-09-410-025-4	Sequence 4, Appli
94	3	27.3	11	3	US-09-133-062D-26	Sequence 26, Appl
95	3	27.3	11	3	US-09-133-062D-29	Sequence 29, Appl
96	3	27.3	11	3	US-09-217-352-206	Sequence 206, App
97	3	27.3	11	4	US-09-302-629-59	Sequence 59, Appl
98	3	27.3	11	4	US-09-455-061-19	Sequence 19, Appl
99	3	27.3	11	4	US-09-025-596-34	Sequence 34, Appl
100	3	27.3	11	4	US-09-115-737-128	Sequence 128, App

# ALIGNMENTS

## RESULT 1

US-08-105-904B-9

; Sequence 9, Application US/08105904B

; Patent No. 6001364

## ; GENERAL INFORMATION:

; APPLICANT: Rose, Keith

; APPLICANT: Offord, Robin

; TITLE OF INVENTION: HETERO-POLYOXIME COMPOUNDS AND THEIR

; TITLE OF INVENTION: PREPARATION BY PARALLEL ASSEMBLY

; NUMBER OF SEQUENCES: 24

## ; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum

; STREET: 5 Palo Alto Square, 3000 El Camino Real

; CITY: Palo Alto

; STATE: California

; COUNTRY: U.S.A.

; ZIP: 94306

## ; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/105,904B  
; FILING DATE: 31-AUG-1993  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/057,594  
; FILING DATE: 05-MAY-1993  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Neeley, Richard L.  
; REGISTRATION NUMBER: 30,092  
; REFERENCE/DOCKET NUMBER: ABIC-001/02US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415)843-5000  
; TELEFAX: (415)857-0663  
; TELEX: 380816 CooleyPA  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: 1  
; OTHER INFORMATION: GXL-Gly  
; FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: 4  
; OTHER INFORMATION: Lys-GXL  
; FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: 5  
; OTHER INFORMATION: Lys-GXL  
; FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: 6  
; OTHER INFORMATION: Lys-GXL  
; FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: 7  
; OTHER INFORMATION: Lys-GXL  
; FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: 8  
; OTHER INFORMATION: Lys-GXL  
; FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: 9  
; OTHER INFORMATION: Lys-GXL  
; FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: 10  
; OTHER INFORMATION: Lys-GXL

US-08-105-904B-9

Query Match 54.5%; Score 6; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.6;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GGK K K K K 8  
      | | | | |  
Db 2 GGK K K K K 7

RESULT 2

US-08-105-904B-21

; Sequence 21, Application US/08105904B  
; Patent No. 6001364  
; GENERAL INFORMATION:  
; APPLICANT: Rose, Keith  
; APPLICANT: Offord, Robin  
; TITLE OF INVENTION: HETERO-POLYOXIME COMPOUNDS AND THEIR  
; TITLE OF INVENTION: PREPARATION BY PARALLEL ASSEMBLY  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum  
; STREET: 5 Palo Alto Square, 3000 El Camino Real  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 94306  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/105,904B  
; FILING DATE: 31-AUG-1993  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/057,594  
; FILING DATE: 05-MAY-1993  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Neeley, Richard L.  
; REGISTRATION NUMBER: 30,092  
; REFERENCE/DOCKET NUMBER: ABIC-001/02US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415)843-5000  
; TELEFAX: (415)857-0663  
; TELEX: 380816 CooleyPA  
; INFORMATION FOR SEQ ID NO: 21:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; FEATURE:

```

; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: Lys-BOC
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 5
; OTHER INFORMATION: Lys-BOC
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 6
; OTHER INFORMATION: Lys-BOC
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 7
; OTHER INFORMATION: Lys-BOC
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 8
; OTHER INFORMATION: Lys-BOC
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 9
; OTHER INFORMATION: Lys-BOC
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 10
; OTHER INFORMATION: Lys-BOC
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 11
; OTHER INFORMATION: Gly-PAM
US-08-105-904B-21

```

```

Query Match          54.5%; Score 6; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches      6; Conservative    0; Mismatches    0; Indels      0; Gaps      0;

```

```

Qy      3 GGK KKK 8
        |||||
Db      2 GGK KKK 7

```

```

RESULT 3
US-08-114-877A-9
; Sequence 9, Application US/08114877A
; Patent No. 6174530
; GENERAL INFORMATION:
; APPLICANT: Rose, Keith
; APPLICANT: Offord, Robin
; TITLE OF INVENTION: HOMOGENOUS POLYOXIME COMPOSITIONS AND THEIR
; TITLE OF INVENTION: PREPARATION BY PARALLEL ASSEMBLY
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
; STREET: 5 Palo Alto Square
; CITY: Palo Alto
; STATE: California

```



; COUNTRY: U.S.A.  
; ZIP: 94036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/114,877A  
; FILING DATE: 31-AUG-1993  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/057,594  
; FILING DATE: 05-MAY-1993  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Neeley, Richard L.  
; REGISTRATION NUMBER: 30,092  
; REFERENCE/DOCKET NUMBER: ABIC-001/01US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 843 5070  
; TELEFAX: (415) 857-0663  
; TELEX: 380816 CooleyPA  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: 1  
; OTHER INFORMATION: GLX-Gly  
; FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: 4  
; OTHER INFORMATION: Lys-GLX  
; FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: 5  
; OTHER INFORMATION: Lys-GLX  
; FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: 6  
; OTHER INFORMATION: Lys-GLX  
; FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: 7  
; OTHER INFORMATION: Lys-GLX  
; FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: 8  
; OTHER INFORMATION: Lys-GLX  
; FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: 9

; OTHER INFORMATION: Lys-GLX  
; FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: 10  
; OTHER INFORMATION: Lys-GLX  
US-08-114-877A-9

Query Match 54.5%; Score 6; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.6;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GGK K K K K 8  
| | | | |  
Db 2 GGK K K K K 7

RESULT 4

US-08-114-877A-14

; Sequence 14, Application US/08114877A  
; Patent No. 6174530

; GENERAL INFORMATION:

; APPLICANT: Rose, Keith  
; APPLICANT: Offord, Robin  
; TITLE OF INVENTION: HOMOGENOUS POLYOXIME COMPOSITIONS AND THEIR  
; TITLE OF INVENTION: PREPARATION BY PARALLEL ASSEMBLY  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum  
; STREET: 5 Palo Alto Square  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 94036

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/114,877A  
; FILING DATE: 31-AUG-1993  
; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/057,594  
; FILING DATE: 05-MAY-1993  
; CLASSIFICATION: 424

; ATTORNEY/AGENT INFORMATION:

; NAME: Neeley, Richard L.  
; REGISTRATION NUMBER: 30,092  
; REFERENCE/DOCKET NUMBER: ABIC-001/01US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 843 5070  
; TELEFAX: (415) 857-0663  
; TELEX: 380816 CooleyPA

; INFORMATION FOR SEQ ID NO: 14:

; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids

```

;     TYPE:  amino acid
;     TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
;     HYPOTHETICAL:  NO
;     FEATURE:
;       NAME/KEY:  Modified-site
;       LOCATION:  4
;       OTHER INFORMATION:  Lys-BOC
;     FEATURE:
;       NAME/KEY:  Modified-site
;       LOCATION:  5
;       OTHER INFORMATION:  Lys-BOC
;     FEATURE:
;       NAME/KEY:  Modified-site
;       LOCATION:  6
;       OTHER INFORMATION:  Lys-BOC
;     FEATURE:
;       NAME/KEY:  Modified-site
;       LOCATION:  7
;       OTHER INFORMATION:  Lys-BOC
;     FEATURE:
;       NAME/KEY:  Modified-site
;       LOCATION:  8
;       OTHER INFORMATION:  Lys-BOC
;     FEATURE:
;       NAME/KEY:  Modified-site
;       LOCATION:  9
;       OTHER INFORMATION:  Lys-BOC
;     FEATURE:
;       NAME/KEY:  Modified-site
;       LOCATION:  10
;       OTHER INFORMATION:  Lys-BOC
;     FEATURE:
;       NAME/KEY:  Modified-site
;       LOCATION:  11
;       OTHER INFORMATION:  Gly-PAM

```

US-08-114-877A-14

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Query Match          54.5%;  Score 6;  DB 3;  Length 11;
Best Local Similarity 100.0%;  Pred. No. 3.6;
Matches      6;  Conservative    0;  Mismatches    0;  Indels      0;  Gaps      0;

```

```

Qy      3 GGK KKK 8
        |||||
Db      2 GGK KKK 7

```

# RESULT 5

US-07-694-983-15

```

; Sequence 15, Application US/07694983
; Patent No. 5432260
; GENERAL INFORMATION:
;   APPLICANT:  Stahl, Philip D.
;   TITLE OF INVENTION:  HIGH AFFINITY MANNOSE RECEPTOR
;   TITLE OF INVENTION:  LIGANDS
;   NUMBER OF SEQUENCES:  19
;   CORRESPONDENCE ADDRESS:

```

```

;   ADDRESSEE:  Irell & Manella
;   STREET:    545 Middlefield Road, Suite 200
;   CITY:      Menlo Park
;   STATE:     California
;   COUNTRY:   USA
;   ZIP:       94025
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE:  Floppy disk
;   COMPUTER:    IBM PC compatible
;   OPERATING SYSTEM:  PC-DOS/MS-DOS
;   SOFTWARE:    PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  US/07/694,983
;   FILING DATE:    19910503
;   CLASSIFICATION:  530
;   ATTORNEY/AGENT INFORMATION:
;   NAME:         Murashige, Kate H.
;   REGISTRATION NUMBER:  29,959
;   REFERENCE/DOCKET NUMBER:  9500-0039.00
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE:    415-327-7250
;   TELEFAX:     415-327-2951
;   TELEX:       706141
;   INFORMATION FOR SEQ ID NO:  15:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH:      11 amino acids
;   TYPE:        AMINO ACID
;   STRANDEDNESS:  single
;   TOPOLOGY:    linear
;   MOLECULE TYPE:  peptide
;   FEATURE:
;   NAME/KEY:    Peptide
;   LOCATION:    1
;   OTHER INFORMATION:  /label= Ac-
;   FEATURE:
;   NAME/KEY:    Peptide
;   LOCATION:    11
;   OTHER INFORMATION:  /label= -NH2
US-07-694-983-15

```

```

Query Match          36.4%;  Score 4;  DB 1;  Length 11;
Best Local Similarity 100.0%;  Pred. No. 3.5e+02;
Matches      4;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

```

```

Qy      5 KKKK 8
        ||||
Db      2 KKKK 5

```

```

RESULT 6
US-08-592-500-39
; Sequence 39, Application US/08592500
; Patent No. 6005089
; GENERAL INFORMATION:
;   APPLICANT:  Lanza, Francois
;   APPLICANT:  Phillips, David R.
;   APPLICANT:  Cazenave, Jean-Pierre

```

```

; TITLE OF INVENTION: Platelet Glycoprotein V Gene and Uses
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/592,500
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/089,455
; FILING DATE: 09-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Karen B.
; REGISTRATION NUMBER: 29,684
; REFERENCE/DOCKET NUMBER: 12418-28
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..11
; OTHER INFORMATION: /note= "Amino acid sequence of the
; OTHER INFORMATION: human fibrinogen (Fg) A-alpha 1 chain thrombin
; OTHER INFORMATION: cleavage site."
; FEATURE:
; NAME/KEY: Region
; LOCATION: 1..2
; OTHER INFORMATION: /note= "Amino acid residues
; OTHER INFORMATION: identical to GPV."
; FEATURE:
; NAME/KEY: Region
; LOCATION: 5
; OTHER INFORMATION: /note= "Amino acid residue
; OTHER INFORMATION: identical to GPV."
; FEATURE:
; NAME/KEY: Region
; LOCATION: 7..9
; OTHER INFORMATION: /note= "Amino acid residues
; OTHER INFORMATION: identical to GPV."
US-08-592-500-39

```

Query Match 36.4%; Score 4; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEGG 4  
||||  
Db 1 AEGG 4

RESULT 7

US-08-970-833-8

; Sequence 8, Application US/08970833

; Patent No. 6022859

; GENERAL INFORMATION:

; APPLICANT: Kiessling, Laura L.

; APPLICANT: Murphy, Regina M.

; TITLE OF INVENTION: INHIBITORS OF BETA-AMYLOID TOXICITY

; NUMBER OF SEQUENCES: 11

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Quarles & Brady

; STREET: 411 East Wisconsin Avenue

; CITY: Milwaukee

; STATE: Wisconsin

; COUNTRY: U.S.A.

; ZIP: 53202-4497

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/970,833

; FILING DATE:

; CLASSIFICATION: 530

; ATTORNEY/AGENT INFORMATION:

; NAME: Baker, Jean C.

; REGISTRATION NUMBER: 35,433

; REFERENCE/DOCKET NUMBER: 960296.94291

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (414) 277-5709

; TELEFAX: (414) 271-3552

; INFORMATION FOR SEQ ID NO: 8:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-970-833-8

Query Match 36.4%; Score 4; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KKKK 8  
||||

## RESULT 8

US-08-195-006-39

; Sequence 39, Application US/08195006

; Patent No. 6083688

## ; GENERAL INFORMATION:

; APPLICANT: Lanza, Francois

; APPLICANT: Phillips, David R.

; APPLICANT: Cazenave, Jean-Pierre

; TITLE OF INVENTION: Platelet Glycoprotein V Gene and Uses

; NUMBER OF SEQUENCES: 43

## ; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend Kourie and Crew

; STREET: 379 Lytton Avenue

; CITY: Palo Alto

; STATE: California

; COUNTRY: US

; ZIP: 94301

## ; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

## ; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/195,006

; FILING DATE: 10-FEB-1994

; CLASSIFICATION: 514

## ; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/089,455

; FILING DATE: 09-JUL-1993

## ; ATTORNEY/AGENT INFORMATION:

; NAME: Dow, Karen B.

; REGISTRATION NUMBER: 29,684

; REFERENCE/DOCKET NUMBER: 12418-28

## ; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 326-2400

; TELEFAX: (415) 326-2422

## ; INFORMATION FOR SEQ ID NO: 39:

## ; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids

; TYPE: amino acid

; TOPOLOGY: unknown

; MOLECULE TYPE: peptide

; HYPOTHETICAL: NO

## ; FEATURE:

; NAME/KEY: Peptide

; LOCATION: 1..11

; OTHER INFORMATION: /note= "Amino acid sequence of the

; OTHER INFORMATION: human fibrinogen (Fg) A-alpha 1 chain thrombin

; OTHER INFORMATION: cleavage site."

## ; FEATURE:

; NAME/KEY: Region

; LOCATION: 1..2

; OTHER INFORMATION: /note= "Amino acid residues

; OTHER INFORMATION: identical to GPV."

```

; FEATURE:
;   NAME/KEY: Region
;   LOCATION: 5
;   OTHER INFORMATION: /note= "Amino acid residue
;   OTHER INFORMATION: identical to GPV."
; FEATURE:
;   NAME/KEY: Region
;   LOCATION: 7..9
;   OTHER INFORMATION: /note= "Amino acid residues
;   OTHER INFORMATION: identical to GPV."
US-08-195-006-39

```

```

Query Match          36.4%; Score 4; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches      4; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      1 AEGG 4
        ||||
Db      1 AEGG 4

```

RESULT 9

US-08-584-043A-5

; Sequence 5, Application US/08584043A

; Patent No. 6344436

; GENERAL INFORMATION:

; APPLICANT: Smith, Louis C.

; APPLICANT: Sparrow, James T.

; APPLICANT: Hauer, Jochen

; APPLICANT: Mims, Martha P.

; TITLE OF INVENTION: LIPOPHILIC PEPTIDES FOR

; TITLE OF INVENTION: MACROMOLECULE DELIVERY

; NUMBER OF SEQUENCES: 139

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon & Lyon

; STREET: 633 West Fifth Street

; STREET: Suite 4700

; CITY: Los Angeles

; STATE: California

; COUNTRY: U.S.A.

; ZIP: 90071-2066

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; MEDIUM TYPE: storage

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: IBM P.C. DOS 6.0

; SOFTWARE: Word Perfect 6.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/584,043A

; FILING DATE: January 8, 1996

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Warburg, Richard J.

; REGISTRATION NUMBER: 32,327



; REFERENCE/DOCKET NUMBER: 217/189  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-584-043A-5

Query Match 36.4%; Score 4; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KKKK 8  
|||  
Db 1 KKKK 4

RESULT 10

US-08-584-043A-43

; Sequence 43, Application US/08584043A  
; Patent No. 6344436  
; GENERAL INFORMATION:  
; APPLICANT: Smith, Louis C.  
; APPLICANT: Sparrow, James T.  
; APPLICANT: Hauer, Jochen  
; APPLICANT: Mims, Martha P.  
; TITLE OF INVENTION: LIPOPHILIC PEPTIDES FOR  
; TITLE OF INVENTION: MACROMOLECULE DELIVERY  
; NUMBER OF SEQUENCES: 139  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; STREET: Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071-2066  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 6.0  
; SOFTWARE: Word Perfect 6.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/584,043A  
; FILING DATE: January 8, 1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:

; NAME: Warburg, Richard J.  
 ; REGISTRATION NUMBER: 32,327  
 ; REFERENCE/DOCKET NUMBER: 217/189  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (213) 489-1600  
 ; TELEFAX: (213) 955-0440  
 ; TELEX: 67-3510  
 ; INFORMATION FOR SEQ ID NO: 43:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 11 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 ; FEATURE:  
 ; OTHER INFORMATION: "Xaa" stands for any naturally  
 ; OTHER INFORMATION: occurring amino acid and  
 ; OTHER INFORMATION: analogues thereof.  
 US-08-584-043A-43

Query Match 36.4%; Score 4; DB 4; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KKKK 8  
 ||||  
 Db 1 KKKK 4

# RESULT 11

US-08-584-043A-99  
 ; Sequence 99, Application US/08584043A  
 ; Patent No. 6344436  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Smith, Louis C.  
 ; APPLICANT: Sparrow, James T.  
 ; APPLICANT: Hauer, Jochen  
 ; APPLICANT: Mims, Martha P.  
 ; TITLE OF INVENTION: LIPOPHILIC PEPTIDES FOR  
 ; TITLE OF INVENTION: MACROMOLECULE DELIVERY  
 ; NUMBER OF SEQUENCES: 139  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Lyon & Lyon  
 ; STREET: 633 West Fifth Street  
 ; STREET: Suite 4700  
 ; CITY: Los Angeles  
 ; STATE: California  
 ; COUNTRY: U.S.A.  
 ; ZIP: 90071-2066  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
 ; MEDIUM TYPE: storage  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: IBM P.C. DOS 6.0  
 ; SOFTWARE: Word Perfect 6.1  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/584,043A

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; FILING DATE: January 8, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 217/189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 99:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-584-043A-99

```

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Query Match          36.4%; Score 4; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches      4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

Qy      5 KKKK 8
        ||||
Db      1 KKKK 4

```

# RESULT 12

```

US-09-082-358B-11
; Sequence 11, Application US/09082358B
; Patent No. 6469153
; GENERAL INFORMATION:
; APPLICANT: Goff, Stephen P.
; APPLICANT: Li, Xingquiang
; TITLE OF INVENTION: EIP-1, EIP-3 GENES, ENVELOPE-INTERACTING PROTEINS,
; TITLE OF INVENTION: EIP-1, and EIP-3
; FILE REFERENCE: 0575/54804
; CURRENT APPLICATION NUMBER: US/09/082,358B
; CURRENT FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 11
; TYPE: PRT
; ORGANISM: murine
US-09-082-358B-11

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```

Query Match          36.4%; Score 4; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches      4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      5 KKKK 8
        ||||

```

Db 1 KKKK 4

RESULT 13

US-09-579-664B-33

; Sequence 33, Application US/09579664B  
; Patent No. 6514719  
; GENERAL INFORMATION:  
; APPLICANT: Immunex Corporation  
; APPLICANT: Bird, Timothy A.  
; APPLICANT: Virca, G. Duke  
; APPLICANT: Martin, Unja  
; APPLICANT: Anderson, Dirk M.  
; TITLE OF INVENTION: NOVEL MURINE AND HUMAN KINASES  
; FILE REFERENCE: 2923-A  
; CURRENT APPLICATION NUMBER: US/09/579,664B  
; CURRENT FILING DATE: 2000-05-26  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 33  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: peptide  
US-09-579-664B-33

Query Match 36.4%; Score 4; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KKKK 8

||||

Db 1 KKKK 4

RESULT 14

PCT-US94-07644A-39

; Sequence 39, Application PC/TUS9407644A  
; GENERAL INFORMATION:  
; APPLICANT: COR Therapeutics, Inc.  
; TITLE OF INVENTION: Platelet Glycoprotein V Gene and Uses  
; NUMBER OF SEQUENCES: 43  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend Khourie and Crew  
; STREET: 379 Lytton Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: US  
; ZIP: 94301  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US94/07644A

```

; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Karen B.
; REGISTRATION NUMBER: 29,684
; REFERENCE/DOCKET NUMBER: 012418-003000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..11
; OTHER INFORMATION: /note= "Amino acid sequence of the
; OTHER INFORMATION: human fibrinogen (Fg) A-alpha 1 chain thrombin
; OTHER INFORMATION: cleavage site."
; FEATURE:
; NAME/KEY: Region
; LOCATION: 1..2
; OTHER INFORMATION: /note= "Amino acid residues
; OTHER INFORMATION: identical to GPV."
; FEATURE:
; NAME/KEY: Region
; LOCATION: 5
; OTHER INFORMATION: /note= "Amino acid residue
; OTHER INFORMATION: identical to GPV."
; FEATURE:
; NAME/KEY: Region
; LOCATION: 7..9
; OTHER INFORMATION: /note= "Amino acid residues
; OTHER INFORMATION: identical to GPV."

```

PCT-US94-07644A-39

```

Query Match          36.4%; Score 4; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches      4; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      1 AEGG 4
        ||||
Db      1 AEGG 4

```

RESULT 15  
5219739-40

```

;Patent No. 5219739
; APPLICANT: TISCHER, EDMUND G.;ABRAHAM, JUDITH A.;FIDDES,
;JOHN C.;MITCHELL, RICHARD L.
; TITLE OF INVENTION: DNA SEQUENCES ENCODING BVEGF120 AND
;HVEGF 121 AND METHODS FOR THE PRODUCTION OF BOVINE AND HUMAN
;VAASCULAR ENDOTHELIAL CELL GROWTH FACTORS, BVEGF120 AND HVEGF121
; NUMBER OF SEQUENCES: 40
; CURRENT APPLICATION DATA:

```

; APPLICATION NUMBER: US/07/559,041  
; FILING DATE: 27-JUL-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 450,883  
; FILING DATE: 14-DEC-1989  
; APPLICATION NUMBER: 387,545  
; FILING DATE: 27-JUL-1989  
;SEQ ID NO:40:  
; LENGTH: 11  
5219739-40

Query Match 36.4%; Score 4; DB 6; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEGG 4  
|||  
Db 1 AEGG 4

RESULT 16

US-07-664-989B-17

; Sequence 17, Application US/07664989B

; Patent No. 5223409

; GENERAL INFORMATION:

; APPLICANT: Ladner, Robert Charles

; APPLICANT: Guterman, Sonia Kosow

; APPLICANT: Roberts, Bruce Lindsay

; APPLICANT: Markland, William

; APPLICANT: Ley, Arthur Charles

; APPLICANT: Kent, Rachel Baribault

; TITLE OF INVENTION: Directed Evolution of No. 5223409e1

; TITLE OF INVENTION: Binding Proteins

; NUMBER OF SEQUENCES: 121

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Browdy and Neimark

; STREET: 419 Seventh Street, N.W.

; STREET: Suite 300

; CITY: Washington,

; STATE: DC

; COUNTRY: USA

; ZIP: 20004

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: WORDPERFECT 4.2

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/664,989B

; FILING DATE: 19910301

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/US89/03731

; FILING DATE: 01-SEP-1989

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/487,063

; FILING DATE: 02-MAR-1990

; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/240,160  
; FILING DATE: 02-SEP-1988  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Cooper, Iver P.  
; REGISTRATION NUMBER: 28005  
; REFERENCE/DOCKET NUMBER: LADNER 7  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528  
; INFORMATION FOR SEQ ID NO: 17:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: AMINO ACID  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-07-664-989B-17

Query Match 27.3%; Score 3; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEG 3  
|||  
Db 9 AEG 11

RESULT 17

US-07-718-274A-31

; Sequence 31, Application US/07718274A  
; Patent No. 5284756  
; GENERAL INFORMATION:  
; APPLICANT: Grinna, Lynn  
; APPLICANT: Parsons, Thomas F.  
; APPLICANT: Theofan, Georgia  
; TITLE OF INVENTION: Osteogenic Factor  
; NUMBER OF SEQUENCES: 63  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
; ADDRESSEE: Bicknell  
; STREET: Two First National Plaza, 20 South Clark  
; STREET: Street  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60603  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/718,274A  
; FILING DATE: 19910620  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/415,555

```

; FILING DATE: 04-OCT-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/256,034
; FILING DATE: 11-OCT-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharp, Jeffrey S.
; REGISTRATION NUMBER: 31,879
; REFERENCE/DOCKET NUMBER: 27129/9430
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-718-274A-31

```

```

Query Match          27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

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```

Qy      3 GGK 5
        |||
Db      3 GGK 5

```

RESULT 18

US-08-029-333-4

```

; Sequence 4, Application US/08029333
; Patent No. 5399667
; GENERAL INFORMATION:
; APPLICANT: Frazier, William A.
; APPLICANT: Kosfeld, Minh D.
; TITLE OF INVENTION: Thrombospondin Receptor Binding Peptides
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scott J. Meyer, Monsanto Co., A3SG
; STREET: 800 N. Lindbergh Blvd.
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63167
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/029,333
; FILING DATE: 19930305
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyer, Scott J.
; REGISTRATION NUMBER: 25,275

```



; REFERENCE/DOCKET NUMBER: 07-24(982)A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (314)694-3117  
; TELEFAX: (314)694-5435  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: AMINO ACID  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-029-333-4

Query Match 27.3%; Score 3; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GKK 6  
|||  
Db 9 GKK 11

RESULT 19

US-08-029-333-30  
; Sequence 30, Application US/08029333  
; Patent No. 5399667  
; GENERAL INFORMATION:  
; APPLICANT: Frazier, William A.  
; APPLICANT: Kosfeld, Minh D.  
; TITLE OF INVENTION: Thrombospondin Receptor Binding Peptides  
; NUMBER OF SEQUENCES: 47  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Scott J. Meyer, Monsanto Co., A3SG  
; STREET: 800 N. Lindbergh Blvd.  
; CITY: St. Louis  
; STATE: Missouri  
; COUNTRY: USA  
; ZIP: 63167  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/029,333  
; FILING DATE: 19930305  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meyer, Scott J.  
; REGISTRATION NUMBER: 25,275  
; REFERENCE/DOCKET NUMBER: 07-24(982)A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (314)694-3117  
; TELEFAX: (314)694-5435  
; INFORMATION FOR SEQ ID NO: 30:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: AMINO ACID

; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-029-333-30

Query Match 27.3%; Score 3; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GKK 6  
|||  
Db 9 GKK 11

RESULT 20

US-08-029-333-32

; Sequence 32, Application US/08029333  
; Patent No. 5399667  
; GENERAL INFORMATION:  
; APPLICANT: Frazier, William A.  
; APPLICANT: Kosfeld, Minh D.  
; TITLE OF INVENTION: Thrombospondin Receptor Binding Peptides  
; NUMBER OF SEQUENCES: 47  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Scott J. Meyer, Monsanto Co., A3SG  
; STREET: 800 N. Lindbergh Blvd.  
; CITY: St. Louis  
; STATE: Missouri  
; COUNTRY: USA  
; ZIP: 63167  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/029,333  
; FILING DATE: 19930305  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meyer, Scott J.  
; REGISTRATION NUMBER: 25,275  
; REFERENCE/DOCKET NUMBER: 07-24(982)A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (314)694-3117  
; TELEFAX: (314)694-5435  
; INFORMATION FOR SEQ ID NO: 32:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: AMINO ACID  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-029-333-32

Query Match 27.3%; Score 3; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GKK 6  
|||  
Db 9 GKK 11

RESULT 21

US-08-029-333-33

; Sequence 33, Application US/08029333  
; Patent No. 5399667  
; GENERAL INFORMATION:  
; APPLICANT: Frazier, William A.  
; APPLICANT: Kosfeld, Minh D.  
; TITLE OF INVENTION: Thrombospondin Receptor Binding Peptides  
; NUMBER OF SEQUENCES: 47  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Scott J. Meyer, Monsanto Co., A3SG  
; STREET: 800 N. Lindbergh Blvd.  
; CITY: St. Louis  
; STATE: Missouri  
; COUNTRY: USA  
; ZIP: 63167  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/029,333  
; FILING DATE: 19930305  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meyer, Scott J.  
; REGISTRATION NUMBER: 25,275  
; REFERENCE/DOCKET NUMBER: 07-24(982)A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (314)694-3117  
; TELEFAX: (314)694-5435  
; INFORMATION FOR SEQ ID NO: 33:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: AMINO ACID  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide

US-08-029-333-33

Query Match 27.3%; Score 3; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GKK 6  
|||  
Db 9 GKK 11

RESULT 22

US-08-029-333-46

; Sequence 46, Application US/08029333

```

; Patent No. 5399667
; GENERAL INFORMATION:
;   APPLICANT: Frazier, William A.
;   APPLICANT: Kosfeld, Minh D.
;   TITLE OF INVENTION: Thrombospondin Receptor Binding Peptides
;   NUMBER OF SEQUENCES: 47
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Scott J. Meyer, Monsanto Co., A3SG
;     STREET: 800 N. Lindbergh Blvd.
;     CITY: St. Louis
;     STATE: Missouri
;     COUNTRY: USA
;     ZIP: 63167
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/029,333
;     FILING DATE: 19930305
;     CLASSIFICATION: 530
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Meyer, Scott J.
;     REGISTRATION NUMBER: 25,275
;     REFERENCE/DOCKET NUMBER: 07-24(982)A
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (314)694-3117
;     TELEFAX: (314)694-5435
;   INFORMATION FOR SEQ ID NO: 46:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 11 amino acids
;       TYPE: AMINO ACID
;       TOPOLOGY: linear
;     MOLECULE TYPE: peptide
US-08-029-333-46

```

```

Query Match          27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      4 GKK 6
      |||
Db      9 GKK 11

```

```

RESULT 23
US-08-149-106-31
; Sequence 31, Application US/08149106
; Patent No. 5411941
; GENERAL INFORMATION:
;   APPLICANT: Grinna, Lynn
;   APPLICANT: Parsons, Thomas F.
;   APPLICANT: Theofan, Georgia
;   TITLE OF INVENTION: Osteogenic Factor
;   NUMBER OF SEQUENCES: 63
;   CORRESPONDENCE ADDRESS:

```

; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
; ADDRESSEE: Bicknell  
; STREET: Two First National Plaza, 20 South Clark  
; STREET: Street  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60603

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/149,106  
; FILING DATE:  
; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/415,555  
; FILING DATE: 04-OCT-1989

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/256,034  
; FILING DATE: 11-OCT-1988

; ATTORNEY/AGENT INFORMATION:

; NAME: Sharp, Jeffrey S.  
; REGISTRATION NUMBER: 31,879  
; REFERENCE/DOCKET NUMBER: 27129/9430

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (312) 346-5750  
; TELEFAX: (312) 984-9740  
; TELEX: 25-3856

; INFORMATION FOR SEQ ID NO: 31:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-149-106-31

Query Match 27.3%; Score 3; DB 1; Length 11;

Best Local Similarity 100.0%; Pred. No. 3.4e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 G GK 5

|||

Db 3 G GK 5

RESULT 24

US-07-603-675-8

; Sequence 8, Application US/07603675

; Patent No. 5416006

; GENERAL INFORMATION:

; APPLICANT: Blasi, Francesco  
; APPLICANT: Stoppelli, Maria P  
; APPLICANT: Mastronicola, Maria R  
; APPLICANT: Welinder, Karen G

; APPLICANT: Correas, Isabel  
 ; TITLE OF INVENTION: MODIFICATION OF PLASMINOGEN ACTIVATORS  
 ; NUMBER OF SEQUENCES: 8  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: COOPER & DUNHAM  
 ; STREET: 30 ROCKEFELLER PLAZA  
 ; CITY: NEW YORK  
 ; STATE: NEW YORK  
 ; COUNTRY: U.S.A.  
 ; ZIP: 10112  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.24  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/07/603,675  
 ; FILING DATE: 19911218  
 ; CLASSIFICATION: 514  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/DK90/00096  
 ; FILING DATE: 11-APR-1990  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: White, John P  
 ; REGISTRATION NUMBER: 28,678  
 ; REFERENCE/DOCKET NUMBER: 38154  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (212) 977-9550  
 ; TELEFAX: (212) 644-0525  
 ; TELEX: (212) 422523 COOP UI  
 ; INFORMATION FOR SEQ ID NO: 8:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 11 amino acids  
 ; TYPE: AMINO ACID  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 ; HYPOTHETICAL: N  
 ; FRAGMENT TYPE: internal  
 US-07-603-675-8

Query Match 27.3%; Score 3; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 3.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GKK 6  
 |||  
 Db 2 GKK 4

RESULT 25  
 US-08-127-278-6  
 ; Sequence 6, Application US/08127278  
 ; Patent No. 5498697  
 ; GENERAL INFORMATION:  
 ; APPLICANT: IWAKI, Kanso  
 ; APPLICANT: OHTA, Tsunetaka  
 ; APPLICANT: KURIOTO, Masahi

```

; TITLE OF INVENTION: PROTEIN, DNA CODING SAID PROTEIN, AND
; TITLE OF INVENTION: PREPARATION OF SAID PROTEIN
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/127,278
; FILING DATE: 27-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 281136/1992
; FILING DATE: 28-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: NEIMARK, Sheridan
; REGISTRATION NUMBER: 20,520
; REFERENCE/DOCKET NUMBER: IWAKI=2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-127-278-6

```

```

Query Match          27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      2 EGG 4
      |||
Db      2 EGG 4

```

# RESULT 26

US-08-298-021-31

```

; Sequence 31, Application US/08298021
; Patent No. 5508263
; GENERAL INFORMATION:
; APPLICANT: Grinna, Lynn
; APPLICANT: Parsons, Thomas F.
; APPLICANT: Theofan, Georgia
; TITLE OF INVENTION: Heterodimeric Osteogenic Factor
; NUMBER OF SEQUENCES: 63

```

```

;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray & Borun
;   STREET:    6300 Sears Tower, 233 South Wacker Drive
;   CITY:     Chicago
;   STATE:    Illinois
;   COUNTRY:   United States of America
;   ZIP:      60606-64023
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE:  Floppy disk
;   COMPUTER:   IBM PC compatible
;   OPERATING SYSTEM:  PC-DOS/MS-DOS
;   SOFTWARE:   PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  US/08/298,021
;   FILING DATE:
;   CLASSIFICATION:  514
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  US 08/149,106
;   FILING DATE:  11-OCT-1993
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  US 07/718,274
;   FILING DATE:  20-JUN-1991
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  US 07/415,555
;   FILING DATE:  04-OCT-1989
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  US 07/256,034
;   FILING DATE:  11-OCT-1988
;   ATTORNEY/AGENT INFORMATION:
;   NAME:  Sharp, Jeffrey S.
;   REGISTRATION NUMBER:  31,879
;   REFERENCE/DOCKET NUMBER:  27129/32196
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  312/474-6300
;   TELEFAX:  312/474-0448
;   TELEX:  25-3856
;   INFORMATION FOR SEQ ID NO:  31:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH:  11 amino acids
;   TYPE:  amino acid
;   TOPOLOGY:  linear
;   MOLECULE TYPE:  protein
US-08-298-021-31

```

```

Query Match          27.38;  Score 3;  DB 1;  Length 11;
Best Local Similarity 100.0%;  Pred. No. 3.4e+03;
Matches      3;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

```

```

Qy      3 GGK 5
      |||
Db      3 GGK 5

```

```

RESULT 27
US-08-211-942-18
; Sequence 18, Application US/08211942
; Patent No. 5523287

```



```

; GENERAL INFORMATION:
;   APPLICANT: Friedrich, Thomas
;   APPLICANT: Bialojan, Siegfried
;   APPLICANT: Kroeger, Burkhard
;   APPLICANT: Kuenast, Christoph
;   TITLE OF INVENTION: No. 5523287el thrombin-inhibitory protein from
assassin
;   TITLE OF INVENTION: bugs.
;   NUMBER OF SEQUENCES: 22
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Keil & Weinkauff
;     STREET: 1101 Connecticut Avenue
;     CITY: Washington
;     STATE: D.C.
;     COUNTRY: USA
;     ZIP: 20036
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage
;     COMPUTER: IBM AT-compatible, 80486 processor
;     OPERATING SYSTEM: MS-DOS version 6.0
;     SOFTWARE: WordPerfect version 5.1
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/211,942
;     FILING DATE:
;     CLASSIFICATION: 435
;     CLASSIFICATION: C07K 13/00
;     CLASSIFICATION: A61K 37/64
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: PCT/EP92/02450
;     FILING DATE: 27-OCT-1992
;   INFORMATION FOR SEQ ID NO: 18:
;     SEQUENCE CHARACTERISTICS:
;     LENGTH: 11 amino acids
;     TYPE: amino acid
;     TOPOLOGY: linear
US-08-211-942-18

```

```

Query Match          27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      2 EGG 4
      |||
Db      1 EGG 3

```

# RESULT 28

US-08-178-570-75

```

; Sequence 75, Application US/08178570
; Patent No. 5532167
; GENERAL INFORMATION:
;   APPLICANT: Lewis C. Cantley
;   APPLICANT: Zhou Song yang
;   TITLE OF INVENTION: Substrate Specificity of Protein Kinases
;   NUMBER OF SEQUENCES: 77
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: LAHIVE & COCKFIELD

```

```

; STREET: 60 STATE STREET, suite 510
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/178,570
; FILING DATE: JANUARY 7, 1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A., Jr.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: BBI-004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 75:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-178-570-75

```

```

Query Match          27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      5 KKK 7
      |||
Db      8 KKK 10

```

# RESULT 29

US-08-146-152-5

```

; Sequence 5, Application US/08146152
; Patent No. 5580956
; GENERAL INFORMATION:
; APPLICANT: SAITO, Hiromitsu
; APPLICANT: ISHIKAWA, Genkichi
; APPLICANT: YAMASAKI, Motoo
; APPLICANT: HONMA, Yoshimi
; TITLE OF INVENTION: PHOSPHOLIPASE C-INHIBITING PEPTIDES
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ANTONELLI, TERRY, STOUT & KRAUS
; STREET: Suite 600, 1919 Pennsylvania Avenue, N.W.
; CITY: Washington,
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20006

```

```

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette - 3.50 inch, 720 Kb storage
; COMPUTER: NEC PC-9801 Seriese
; OPERATING SYSTEM: MS-DOS Ver3.30 or Later
; SOFTWARE:
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/146,152
; FILING DATE: 10-NOV-1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP52394/92
; FILING DATE: 11-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Terry, David T.
; REGISTRATION NUMBER: 20178
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-828-0300
; TELEFAX: 202-828-0380
; TELEX: 440280
; INFORMATION FOR SEQ ID NO: 5 :
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-146-152-5

```

```

Query Match          27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      8 KMR 10
      |||
Db      4 KMR 6

```

RESULT 30

US-08-146-152-11

```

; Sequence 11, Application US/08146152
; Patent No. 5580956
; GENERAL INFORMATION:
; APPLICANT: SAITO, Hiromitsu
; APPLICANT: ISHIKAWA, Genkichi
; APPLICANT: YAMASAKI, Motoo
; APPLICANT: HONMA, Yoshimi
; TITLE OF INVENTION: PHOSPHOLIPASE C-INHIBITING PEPTIDES
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ANTONELLI, TERRY, STOUT & KRAUS
; STREET: Suite 600, 1919 Pennsylvania Avenue, N.W.
; CITY: Washington,
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette - 3.50 inch, 720 Kb storage
; COMPUTER: NEC PC-9801 Seriese

```

```

;   OPERATING SYSTEM:  MS-DOS Ver3.30 or Later
;   SOFTWARE:
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  US/08/146,152
;   FILING DATE:  10-NOV-1993
;   CLASSIFICATION:  530
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  JP52394/92
;   FILING DATE:  11-MAR-1992
;   ATTORNEY/AGENT INFORMATION:
;   NAME:  Terry, David T.
;   REGISTRATION NUMBER:  20178
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  202-828-0300
;   TELEFAX:  202-828-0380
;   TELEX:  440280
;   INFORMATION FOR SEQ ID NO:  11 :
;   SEQUENCE CHARACTERISTICS:
;   LENGTH:  11 amino acids
;   TYPE:  amino acid
;   TOPOLOGY:  linear
;   MOLECULE TYPE:  peptide
;   FEATURE:
;   NAME/KEY:  Modified-site
;   LOCATION:  1
;   IDENTIFICATION METHOD:  by experiment
;   OTHER INFORMATION:  Xaa in Location 1 represents N-(n-Butyryl)-
;   OTHER INFORMATION:  L-Leucine.
;   NAME/KEY:  Modified-site
;   LOCATION:  11
;   IDENTIFICATION METHOD:  by experiment
;   OTHER INFORMATION:  Xaa in Location 11 represents L-Valine
;   OTHER INFORMATION:  amide.
US-08-146-152-11

```

```

Query Match          27.3%;  Score 3;  DB 1;  Length 11;
Best Local Similarity 100.0%;  Pred. No. 3.4e+03;
Matches      3;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

```

```

Qy          8 KMR 10
            |||
Db          4 KMR 6

```

```

RESULT 31
US-08-146-152-12
; Sequence 12, Application US/08146152
; Patent No. 5580956
; GENERAL INFORMATION:
; APPLICANT:  SAITO, Hiromitsu
; APPLICANT:  ISHIKAWA, Genkichi
; APPLICANT:  YAMASAKI, Motoo
; APPLICANT:  HONMA, Yoshimi
; TITLE OF INVENTION:  PHOSPHOLIPASE C-INHIBITING PEPTIDES
; NUMBER OF SEQUENCES:  28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE:  ANTONELLI, TERRY, STOUT & KRAUS

```

```

; STREET: Suite 600, 1919 Pennsylvania Avenue, N.W.
; CITY: Washington,
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette - 3.50 inch, 720 Kb storage
; COMPUTER: NEC PC-9801 Seriese
; OPERATING SYSTEM: MS-DOS Ver3.30 or Later
; SOFTWARE:
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/146,152
; FILING DATE: 10-NOV-1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP52394/92
; FILING DATE: 11-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Terry, David T.
; REGISTRATION NUMBER: 20178
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-828-0300
; TELEFAX: 202-828-0380
; TELEX: 440280
; INFORMATION FOR SEQ ID NO: 12 :
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; IDENTIFICATION METHOD: by experiment
; OTHER INFORMATION: Xaa in Location 1 represents N-Coumaly1-L-
; OTHER INFORMATION: Leucine.
; NAME/KEY: Modified-site
; LOCATION: 11
; IDENTIFICATION METHOD: by experiment
; OTHER INFORMATION: Xaa in Location 11 represents L-Valine
; OTHER INFORMATION: amide.
US-08-146-152-12

```

```

Query Match          27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      8 KMR 10
        |||
Db      4 KMR 6

```

```

RESULT 32
US-08-146-152-13
; Sequence 13, Application US/08146152
; Patent No. 5580956
; GENERAL INFORMATION:

```

```

; APPLICANT: SAITO, Hiromitsu
; APPLICANT: ISHIKAWA, Genkichi
; APPLICANT: YAMASAKI, Motoo
; APPLICANT: HONMA, Yoshimi
; TITLE OF INVENTION: PHOSPHOLIPASE C-INHIBITING PEPTIDES
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ANTONELLI, TERRY, STOUT & KRAUS
; STREET: Suite 600, 1919 Pennsylvania Avenue, N.W.
; CITY: Washington,
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette - 3.50 inch, 720 Kb storage
; COMPUTER: NEC PC-9801 Serieese
; OPERATING SYSTEM: MS-DOS Ver3.30 or Later
; SOFTWARE:
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/146,152
; FILING DATE: 10-NOV-1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP52394/92
; FILING DATE: 11-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Terry, David T.
; REGISTRATION NUMBER: 20178
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-828-0300
; TELEFAX: 202-828-0380
; TELEX: 440280
; INFORMATION FOR SEQ ID NO: 13 :
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; IDENTIFICATION METHOD: by experiment
; OTHER INFORMATION: Xaa in Location 1 represents N-(2,3-
; OTHER INFORMATION: Dihydroxybenzoyl)-L-Leucine.
; NAME/KEY: Modified-site
; LOCATION: 11
; IDENTIFICATION METHOD: by experiment
; OTHER INFORMATION: Xaa in Location 11 represents L-Valine
; OTHER INFORMATION: amide.

```

US-08-146-152-13

```

Query Match          27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

Qy 8 KMR 10  
 |||

## RESULT 33

US-08-146-152-14

; Sequence 14, Application US/08146152

; Patent No. 5580956

## ; GENERAL INFORMATION:

; APPLICANT: SAITO, Hiromitsu

; APPLICANT: ISHIKAWA, Genkichi

; APPLICANT: YAMASAKI, Motoo

; APPLICANT: HONMA, Yoshimi

; TITLE OF INVENTION: PHOSPHOLIPASE C-INHIBITING PEPTIDES

; NUMBER OF SEQUENCES: 28

## ; CORRESPONDENCE ADDRESS:

; ADDRESSEE: ANTONELLI, TERRY, STOUT &amp; KRAUS

; STREET: Suite 600, 1919 Pennsylvania Avenue, N.W.

; CITY: Washington,

; STATE: D.C.

; COUNTRY: U.S.A.

; ZIP: 20006

## ; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette - 3.50 inch, 720 Kb storage

; COMPUTER: NEC PC-9801 Serieese

; OPERATING SYSTEM: MS-DOS Ver3.30 or Later

## ; SOFTWARE:

## ; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/146,152

; FILING DATE: 10-NOV-1993

; CLASSIFICATION: 530

## ; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: JP52394/92

; FILING DATE: 11-MAR-1992

## ; ATTORNEY/AGENT INFORMATION:

; NAME: Terry, David T.

; REGISTRATION NUMBER: 20178

## ; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-828-0300

; TELEFAX: 202-828-0380

; TELEX: 440280

## ; INFORMATION FOR SEQ ID NO: 14 :

## ; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

## ; FEATURE:

; NAME/KEY: Modified-site

; LOCATION: 1

; IDENTIFICATION METHOD: by experiment

; OTHER INFORMATION: Xaa in Location 1 represents N-(2,4-

; OTHER INFORMATION: Dihydroxybenzoyl)-L-Leucine.

; NAME/KEY: Modified-site

; LOCATION: 11

; IDENTIFICATION METHOD: by experiment

; OTHER INFORMATION: Xaa in Location 11 represents L-Valine

; OTHER INFORMATION: amide.

US-08-146-152-14

Query Match 27.3%; Score 3; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KMR 10

|||

Db 4 KMR 6

RESULT 34

US-08-146-152-15

; Sequence 15, Application US/08146152

; Patent No. 5580956

; GENERAL INFORMATION:

; APPLICANT: SAITO, Hiromitsu

; APPLICANT: ISHIKAWA, Genkichi

; APPLICANT: YAMASAKI, Motoo

; APPLICANT: HONMA, Yoshimi

; TITLE OF INVENTION: PHOSPHOLIPASE C-INHIBITING PEPTIDES

; NUMBER OF SEQUENCES: 28

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: ANTONELLI, TERRY, STOUT & KRAUS

; STREET: Suite 600, 1919 Pennsylvania Avenue, N.W.

; CITY: Washington,

; STATE: D.C.

; COUNTRY: U.S.A.

; ZIP: 20006

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette - 3.50 inch, 720 Kb storage

; COMPUTER: NEC PC-9801 Seriese

; OPERATING SYSTEM: MS-DOS Ver3.30 or Later

; SOFTWARE:

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/146,152

; FILING DATE: 10-NOV-1993

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: JP52394/92

; FILING DATE: 11-MAR-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Terry, David T.

; REGISTRATION NUMBER: 20178

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-828-0300

; TELEFAX: 202-828-0380

; TELEX: 440280

; INFORMATION FOR SEQ ID NO: 15 :

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; FEATURE:

; NAME/KEY: Modified-site

; LOCATION: 1



```

; IDENTIFICATION METHOD:  by experiment
; OTHER INFORMATION:  Xaa in Location 1 represents N-(2,5-
; OTHER INFORMATION:  Dihydroxybenzoyl)-L-Leucine.
; NAME/KEY:  Modified-site
; LOCATION:  11
; IDENTIFICATION METHOD:  by experiment
; OTHER INFORMATION:  Xaa in Location 11 represents L-Valine
; OTHER INFORMATION:  amide.

```

US-08-146-152-15

```

Query Match          27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy          8 KMR 10
            |||
Db          4 KMR 6

```

# RESULT 35

US-08-146-152-16

```

; Sequence 16, Application US/08146152
; Patent No. 5580956
; GENERAL INFORMATION:
; APPLICANT:  SAITO, Hiromitsu
; APPLICANT:  ISHIKAWA, Genkichi
; APPLICANT:  YAMASAKI, Motoo
; APPLICANT:  HONMA, Yoshimi
; TITLE OF INVENTION:  PHOSPHOLIPASE C-INHIBITING PEPTIDES
; NUMBER OF SEQUENCES:  28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE:  ANTONELLI, TERRY, STOUT & KRAUS
; STREET:  Suite 600, 1919 Pennsylvania Avenue, N.W.
; CITY:  Washington,
; STATE:  D.C.
; COUNTRY:  U.S.A.
; ZIP:  20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE:  Diskette - 3.50 inch, 720 Kb storage
; COMPUTER:  NEC PC-9801 Serieese
; OPERATING SYSTEM:  MS-DOS Ver3.30 or Later
; SOFTWARE:
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER:  US/08/146,152
; FILING DATE:  10-NOV-1993
; CLASSIFICATION:  530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:  JP52394/92
; FILING DATE:  11-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME:  Terry, David T.
; REGISTRATION NUMBER:  20178
; TELECOMMUNICATION INFORMATION:
; TELEPHONE:  202-828-0300
; TELEFAX:  202-828-0380
; TELEX:  440280
; INFORMATION FOR SEQ ID NO:  16 :

```

```

; SEQUENCE CHARACTERISTICS:
;   LENGTH: 11 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
;   NAME/KEY: Modified-site
;   LOCATION: 1
;   IDENTIFICATION METHOD: by experiment
;   OTHER INFORMATION: Xaa in Location 1 represents N-(3-
;   OTHER INFORMATION: Cyclohexylpropionyl)-L-Leucine.
;   NAME/KEY: Modified-site
;   LOCATION: 11
;   IDENTIFICATION METHOD: by experiment
;   OTHER INFORMATION: Xaa in Location 11 represents L-Valine
;   OTHER INFORMATION: amide.
US-08-146-152-16

```

```

Query Match          27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      8 KMR 10
        |||
Db      4 KMR 6

```

# RESULT 36

US-08-146-152-17

```

; Sequence 17, Application US/08146152
; Patent No. 5580956
; GENERAL INFORMATION:
;   APPLICANT: SAITO, Hiromitsu
;   APPLICANT: ISHIKAWA, Genkichi
;   APPLICANT: YAMASAKI, Motoo
;   APPLICANT: HONMA, Yoshimi
;   TITLE OF INVENTION: PHOSPHOLIPASE C-INHIBITING PEPTIDES
;   NUMBER OF SEQUENCES: 28
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: ANTONELLI, TERRY, STOUT & KRAUS
;   STREET: Suite 600, 1919 Pennsylvania Avenue, N.W.
;   CITY: Washington,
;   STATE: D.C.
;   COUNTRY: U.S.A.
;   ZIP: 20006
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Diskette - 3.50 inch, 720 Kb storage
;   COMPUTER: NEC PC-9801 Serieese
;   OPERATING SYSTEM: MS-DOS Ver3.30 or Later
;   SOFTWARE:
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/146,152
;   FILING DATE: 10-NOV-1993
;   CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: JP52394/92
;   FILING DATE: 11-MAR-1992

```

```

; ATTORNEY/AGENT INFORMATION:
;   NAME: Terry, David T.
;   REGISTRATION NUMBER: 20178
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 202-828-0300
;   TELEFAX: 202-828-0380
;   TELEX: 440280
; INFORMATION FOR SEQ ID NO: 17 :
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 11 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
;   NAME/KEY: Modified-site
;   LOCATION: 1
;   IDENTIFICATION METHOD: by experiment
;   OTHER INFORMATION: Xaa in Location 1 represents N-
;   OTHER INFORMATION: Cyclopentylacetyl-L-Leucine.
;   NAME/KEY: Modified-site
;   LOCATION: 11
;   IDENTIFICATION METHOD: by experiment
;   OTHER INFORMATION: Xaa in Location 11 represents L-Valine
;   OTHER INFORMATION: amide.
US-08-146-152-17

```

```

Query Match          27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      8 KMR 10
        |||
Db      4 KMR 6

```

# RESULT 37

```

US-08-146-152-18
; Sequence 18, Application US/08146152
; Patent No. 5580956
; GENERAL INFORMATION:
;   APPLICANT: SAITO, Hiromitsu
;   APPLICANT: ISHIKAWA, Genkichi
;   APPLICANT: YAMASAKI, Motoo
;   APPLICANT: HONMA, Yoshimi
; TITLE OF INVENTION: PHOSPHOLIPASE C-INHIBITING PEPTIDES
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: ANTONELLI, TERRY, STOUT & KRAUS
;   STREET: Suite 600, 1919 Pennsylvania Avenue, N.W.
;   CITY: Washington,
;   STATE: D.C.
;   COUNTRY: U.S.A.
;   ZIP: 20006
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Diskette - 3.50 inch, 720 Kb storage
;   COMPUTER: NEC PC-9801 Serieese
;   OPERATING SYSTEM: MS-DOS Ver3.30 or Later

```

```

; SOFTWARE:
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/146,152
; FILING DATE: 10-NOV-1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP52394/92
; FILING DATE: 11-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Terry, David T.
; REGISTRATION NUMBER: 20178
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-828-0300
; TELEFAX: 202-828-0380
; TELEX: 440280
; INFORMATION FOR SEQ ID NO: 18 :
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; IDENTIFICATION METHOD: by experiment
; OTHER INFORMATION: Xaa in Location 1 represents N-Propionyl-L-
; OTHER INFORMATION: Leucine.
; NAME/KEY: Modified-site
; LOCATION: 11
; IDENTIFICATION METHOD: by experiment
; OTHER INFORMATION: Xaa in Location 11 represents L-Valine
; OTHER INFORMATION: amide.
US-08-146-152-18

```

```

Query Match          27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      8 KMR 10
      |||
Db      4 KMR 6

```

# RESULT 38

US-08-146-152-19

```

; Sequence 19, Application US/08146152
; Patent No. 5580956
; GENERAL INFORMATION:
; APPLICANT: SAITO, Hiromitsu
; APPLICANT: ISHIKAWA, Genkichi
; APPLICANT: YAMASAKI, Motoo
; APPLICANT: HONMA, Yoshimi
; TITLE OF INVENTION: PHOSPHOLIPASE C-INHIBITING PEPTIDES
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ANTONELLI, TERRY, STOUT & KRAUS
; STREET: Suite 600, 1919 Pennsylvania Avenue, N.W.

```

```

; CITY: Washington,
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette - 3.50 inch, 720 Kb storage
; COMPUTER: NEC PC-9801 Seriese
; OPERATING SYSTEM: MS-DOS Ver3.30 or Later
; SOFTWARE:
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/146,152
; FILING DATE: 10-NOV-1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP52394/92
; FILING DATE: 11-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Terry, David T.
; REGISTRATION NUMBER: 20178
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-828-0300
; TELEFAX: 202-828-0380
; TELEX: 440280
; INFORMATION FOR SEQ ID NO: 19 :
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; IDENTIFICATION METHOD: by experiment
; OTHER INFORMATION: Xaa in Location 1 represents N-Isobutyryl-
; OTHER INFORMATION: L-Leucine.
; NAME/KEY: Modified-site
; LOCATION: 11
; IDENTIFICATION METHOD: by experiment
; OTHER INFORMATION: Xaa in Location 11 represents L-Valine
; OTHER INFORMATION: amide.
US-08-146-152-19

```

```

Query Match          27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      8 KMR 10
      |||
Db      4 KMR 6

```

```

RESULT 39
US-08-146-152-20
; Sequence 20, Application US/08146152
; Patent No. 5580956
; GENERAL INFORMATION:
; APPLICANT: SAITO, Hiromitsu

```

```

; APPLICANT: ISHIKAWA, Genkichi
; APPLICANT: YAMASAKI, Motoo
; APPLICANT: HONMA, Yoshimi
; TITLE OF INVENTION: PHOSPHOLIPASE C-INHIBITING PEPTIDES
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ANTONELLI, TERRY, STOUT & KRAUS
; STREET: Suite 600, 1919 Pennsylvania Avenue, N.W.
; CITY: Washington,
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette - 3.50 inch, 720 Kb storage
; COMPUTER: NEC PC-9801 Serieese
; OPERATING SYSTEM: MS-DOS Ver3.30 or Later
; SOFTWARE:
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/146,152
; FILING DATE: 10-NOV-1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP52394/92
; FILING DATE: 11-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Terry, David T.
; REGISTRATION NUMBER: 20178
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-828-0300
; TELEFAX: 202-828-0380
; TELEX: 440280
; INFORMATION FOR SEQ ID NO: 20 :
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; IDENTIFICATION METHOD: by experiment
; OTHER INFORMATION: Xaa in Location 1 represents N-(2-Ethyl-n-
; OTHER INFORMATION: butyryl)-L-Leucine.
; NAME/KEY: Modified-site
; LOCATION: 11
; IDENTIFICATION METHOD: by experiment
; OTHER INFORMATION: Xaa in Location 11 represents L-Valine
; OTHER INFORMATION: amide.

```

US-08-146-152-20

```

Query Match          27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      8 KMR 10
      |||
Db      4 KMR 6

```

RESULT 40

US-08-146-152-21

; Sequence 21, Application US/08146152

; Patent No. 5580956

; GENERAL INFORMATION:

; APPLICANT: SAITO, Hiromitsu

; APPLICANT: ISHIKAWA, Genkichi

; APPLICANT: YAMASAKI, Motoo

; APPLICANT: HONMA, Yoshimi

; TITLE OF INVENTION: PHOSPHOLIPASE C-INHIBITING PEPTIDES

; NUMBER OF SEQUENCES: 28

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: ANTONELLI, TERRY, STOUT & KRAUS

; STREET: Suite 600, 1919 Pennsylvania Avenue, N.W.

; CITY: Washington,

; STATE: D.C.

; COUNTRY: U.S.A.

; ZIP: 20006

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette - 3.50 inch, 720 Kb storage

; COMPUTER: NEC PC-9801 Seriese

; OPERATING SYSTEM: MS-DOS Ver3.30 or Later

; SOFTWARE:

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/146,152

; FILING DATE: 10-NOV-1993

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: JP52394/92

; FILING DATE: 11-MAR-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Terry, David T.

; REGISTRATION NUMBER: 20178

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-828-0300

; TELEFAX: 202-828-0380

; TELEX: 440280

; INFORMATION FOR SEQ ID NO: 21 :

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; FEATURE:

; NAME/KEY: Modified-site

; LOCATION: 1

; IDENTIFICATION METHOD: by experiment

; OTHER INFORMATION: Xaa in Location 1 represents N-(n-Caprylyl)-

; OTHER INFORMATION: L-Leucine.

; NAME/KEY: Modified-site

; LOCATION: 11

; IDENTIFICATION METHOD: by experiment

; OTHER INFORMATION: Xaa in Location 11 represents L-Valine

; OTHER INFORMATION: amide.

US-08-146-152-21

Query Match 27.3%; Score 3; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KMR 10  
|||  
Db 4 KMR 6

RESULT 41

US-08-146-152-22

; Sequence 22, Application US/08146152

; Patent No. 5580956

; GENERAL INFORMATION:

; APPLICANT: SAITO, Hiromitsu

; APPLICANT: ISHIKAWA, Genkichi

; APPLICANT: YAMASAKI, Motoo

; APPLICANT: HONMA, Yoshimi

; TITLE OF INVENTION: PHOSPHOLIPASE C-INHIBITING PEPTIDES

; NUMBER OF SEQUENCES: 28

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: ANTONELLI, TERRY, STOUT & KRAUS

; STREET: Suite 600, 1919 Pennsylvania Avenue, N.W.

; CITY: Washington,

; STATE: D.C.

; COUNTRY: U.S.A.

; ZIP: 20006

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette - 3.50 inch, 720 Kb storage

; COMPUTER: NEC PC-9801 Serieese

; OPERATING SYSTEM: MS-DOS Ver3.30 or Later

; SOFTWARE:

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/146,152

; FILING DATE: 10-NOV-1993

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: JP52394/92

; FILING DATE: 11-MAR-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Terry, David T.

; REGISTRATION NUMBER: 20178

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-828-0300

; TELEFAX: 202-828-0380

; TELEX: 440280

; INFORMATION FOR SEQ ID NO: 22 :

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; FEATURE:

; NAME/KEY: Modified-site

; LOCATION: 1

; IDENTIFICATION METHOD: by experiment



; OTHER INFORMATION: Xaa in Location 1 represents N-Succinyl-L-  
; OTHER INFORMATION: Leucine.  
; NAME/KEY: Modified-site  
; LOCATION: 11  
; IDENTIFICATION METHOD: by experiment  
; OTHER INFORMATION: Xaa in Location 11 represents L-Valine  
; OTHER INFORMATION: amide.

US-08-146-152-22

Query Match 27.3%; Score 3; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KMR 10  
|||  
Db 4 KMR 6

RESULT 42

US-08-146-152-23

; Sequence 23, Application US/08146152  
; Patent No. 5580956  
; GENERAL INFORMATION:  
; APPLICANT: SAITO, Hiromitsu  
; APPLICANT: ISHIKAWA, Genkichi  
; APPLICANT: YAMASAKI, Motoo  
; APPLICANT: HONMA, Yoshimi  
; TITLE OF INVENTION: PHOSPHOLIPASE C-INHIBITING PEPTIDES  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ANTONELLI, TERRY, STOUT & KRAUS  
; STREET: Suite 600, 1919 Pennsylvania Avenue, N.W.  
; CITY: Washington,  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20006  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette - 3.50 inch, 720 Kb storage  
; COMPUTER: NEC PC-9801 Serieese  
; OPERATING SYSTEM: MS-DOS Ver3.30 or Later  
; SOFTWARE:  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/146,152  
; FILING DATE: 10-NOV-1993  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP52394/92  
; FILING DATE: 11-MAR-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Terry, David T.  
; REGISTRATION NUMBER: 20178  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-828-0300  
; TELEFAX: 202-828-0380  
; TELEX: 440280  
; INFORMATION FOR SEQ ID NO: 23 :  
; SEQUENCE CHARACTERISTICS:

```

;   LENGTH:  11 amino acids
;   TYPE:    amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: peptide
;   FEATURE:
;     NAME/KEY: Modified-site
;     LOCATION: 1
;     IDENTIFICATION METHOD: by experiment
;     OTHER INFORMATION: Xaa in Location 1 represents N-(3-
;     OTHER INFORMATION: Cyclopentylpropionyl)-L-Leucine.
;     NAME/KEY: Modified-site
;     LOCATION: 11
;     IDENTIFICATION METHOD: by experiment
;     OTHER INFORMATION: Xaa in Location 11 represents L-Valine
;     OTHER INFORMATION: amide.

```

US-08-146-152-23

```

Query Match          27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      8 KMR 10
        |||
Db      4 KMR 6

```

#### RESULT 43

US-08-146-152-24

```

; Sequence 24, Application US/08146152
; Patent No. 5580956
; GENERAL INFORMATION:
;   APPLICANT:  SAITO, Hiromitsu
;   APPLICANT:  ISHIKAWA, Genkichi
;   APPLICANT:  YAMASAKI, Motoo
;   APPLICANT:  HONMA, Yoshimi
;   TITLE OF INVENTION:  PHOSPHOLIPASE C-INHIBITING PEPTIDES
;   NUMBER OF SEQUENCES:  28
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  ANTONELLI, TERRY, STOUT & KRAUS
;     STREET:    Suite 600, 1919 Pennsylvania Avenue, N.W.
;     CITY:      Washington,
;     STATE:     D.C.
;     COUNTRY:   U.S.A.
;     ZIP:       20006
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Diskette - 3.50 inch, 720 Kb storage
;     COMPUTER:     NEC PC-9801 Seriese
;     OPERATING SYSTEM:  MS-DOS Ver3.30 or Later
;     SOFTWARE:
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/146,152
;     FILING DATE:        10-NOV-1993
;     CLASSIFICATION:     530
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  JP52394/92
;     FILING DATE:        11-MAR-1992
;   ATTORNEY/AGENT INFORMATION:

```

```

; NAME: Terry, David T.
; REGISTRATION NUMBER: 20178
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-828-0300
; TELEFAX: 202-828-0380
; TELEX: 440280
; INFORMATION FOR SEQ ID NO: 24 :
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; IDENTIFICATION METHOD: by experiment
; OTHER INFORMATION: Xaa in Location 1 represents N-
; OTHER INFORMATION: Cyclopropylcarbonyl-L-Leucine.
; NAME/KEY: Modified-site
; LOCATION: 11
; IDENTIFICATION METHOD: by experiment
; OTHER INFORMATION: Xaa in Location 11 represents L-Valine
; OTHER INFORMATION: amide.
US-08-146-152-24

```

```

Query Match          27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      8 KMR 10
      |||
Db      4 KMR 6

```

#### RESULT 44

US-08-146-152-25

```

; Sequence 25, Application US/08146152
; Patent No. 5580956
; GENERAL INFORMATION:
; APPLICANT: SAITO, Hiromitsu
; APPLICANT: ISHIKAWA, Genkichi
; APPLICANT: YAMASAKI, Motoo
; APPLICANT: HONMA, Yoshimi
; TITLE OF INVENTION: PHOSPHOLIPASE C-INHIBITING PEPTIDES
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ANTONELLI, TERRY, STOUT & KRAUS
; STREET: Suite 600, 1919 Pennsylvania Avenue, N.W.
; CITY: Washington,
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette - 3.50 inch, 720 Kb storage
; COMPUTER: NEC PC-9801 Seriese
; OPERATING SYSTEM: MS-DOS Ver3.30 or Later
; SOFTWARE:

```

```

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/146,152
; FILING DATE: 10-NOV-1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP52394/92
; FILING DATE: 11-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Terry, David T.
; REGISTRATION NUMBER: 20178
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-828-0300
; TELEFAX: 202-828-0380
; TELEX: 440280
; INFORMATION FOR SEQ ID NO: 25 :
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; IDENTIFICATION METHOD: by experiment
; OTHER INFORMATION: Xaa in Location 1 represents N-
; OTHER INFORMATION: Cyclohexylacetyl-L-Leucine.
; NAME/KEY: Modified-site
; LOCATION: 11
; IDENTIFICATION METHOD: by experiment
; OTHER INFORMATION: Xaa in Location 11 represents L-Varine
; OTHER INFORMATION: amide.
US-08-146-152-25

```

```

Query Match          27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      8 KMR 10
      |||
Db      4 KMR 6

```

# RESULT 45

US-08-146-152-26

```

; Sequence 26, Application US/08146152
; Patent No. 5580956
; GENERAL INFORMATION:
; APPLICANT: SAITO, Hiromitsu
; APPLICANT: ISHIKAWA, Genkichi
; APPLICANT: YAMASAKI, Motoo
; APPLICANT: HONMA, Yoshimi
; TITLE OF INVENTION: PHOSPHOLIPASE C-INHIBITING PEPTIDES
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ANTONELLI, TERRY, STOUT & KRAUS
; STREET: Suite 600, 1919 Pennsylvania Avenue, N.W.
; CITY: Washington,

```

```

; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette - 3.50 inch, 720 Kb storage
; COMPUTER: NEC PC-9801 Seriese
; OPERATING SYSTEM: MS-DOS Ver3.30 or Later
; SOFTWARE:
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/146,152
; FILING DATE: 10-NOV-1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP52394/92
; FILING DATE: 11-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Terry, David T.
; REGISTRATION NUMBER: 20178
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-828-0300
; TELEFAX: 202-828-0380
; TELEX: 440280
; INFORMATION FOR SEQ ID NO: 26 :
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; IDENTIFICATION METHOD: by experiment
; OTHER INFORMATION: Xaa in Location 1 represents
; OTHER INFORMATION: N-Cyclopentylcarbonyl-L-Leucine.
; NAME/KEY: Modified-site
; LOCATION: 11
; IDENTIFICATION METHOD: by experiment
; OTHER INFORMATION: Xaa in Location 11 represents L-Valine
; OTHER INFORMATION: amide.
US-08-146-152-26

```

```

Query Match          27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      8 KMR 10
      |||
Db      4 KMR 6

```

```

RESULT 46
US-08-146-152-27
; Sequence 27, Application US/08146152
; Patent No. 5580956
; GENERAL INFORMATION:
; APPLICANT: SAITO, Hiromitsu
; APPLICANT: ISHIKAWA, Genkichi

```

```

; APPLICANT: YAMASAKI, Motoo
; APPLICANT: HONMA, Yoshimi
; TITLE OF INVENTION: PHOSPHOLIPASE C-INHIBITING PEPTIDES
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ANTONELLI, TERRY, STOUT & KRAUS
; STREET: Suite 600, 1919 Pennsylvania Avenue, N.W.
; CITY: Washington,
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette - 3.50 inch, 720 Kb storage
; COMPUTER: NEC PC-9801 Serieese
; OPERATING SYSTEM: MS-DOS Ver3.30 or Later
; SOFTWARE:
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/146,152
; FILING DATE: 10-NOV-1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP52394/92
; FILING DATE: 11-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Terry, David T.
; REGISTRATION NUMBER: 20178
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-828-0300
; TELEFAX: 202-828-0380
; TELEX: 440280
; INFORMATION FOR SEQ ID NO: 27 :
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; IDENTIFICATION METHOD: by experiment
; OTHER INFORMATION: Xaa in Location 1 represents N-(n-Hexanoyl)-
; OTHER INFORMATION: L-Leucine.
; NAME/KEY: Modified-site
; LOCATION: 11
; IDENTIFICATION METHOD: by experiment
; OTHER INFORMATION: Xaa in Location 11 represents L-Valine
; OTHER INFORMATION: amide.
US-08-146-152-27

```

```

Query Match          27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      8 KMR 10
      |||
Db      4 KMR 6

```

RESULT 47  
US-08-146-152-28  
; Sequence 28, Application US/08146152  
; Patent No. 5580956  
; GENERAL INFORMATION:  
; APPLICANT: SAITO, Hiromitsu  
; APPLICANT: ISHIKAWA, Genkichi  
; APPLICANT: YAMASAKI, Motoo  
; APPLICANT: HONMA, Yoshimi  
; TITLE OF INVENTION: PHOSPHOLIPASE C-INHIBITING PEPTIDES  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ANTONELLI, TERRY, STOUT & KRAUS  
; STREET: Suite 600, 1919 Pennsylvania Avenue, N.W.  
; CITY: Washington,  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20006  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette - 3.50 inch, 720 Kb storage  
; COMPUTER: NEC PC-9801 Seriese  
; OPERATING SYSTEM: MS-DOS Ver3.30 or Later  
; SOFTWARE:  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/146,152  
; FILING DATE: 10-NOV-1993  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP52394/92  
; FILING DATE: 11-MAR-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Terry, David T.  
; REGISTRATION NUMBER: 20178  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-828-0300  
; TELEFAX: 202-828-0380  
; TELEX: 440280  
; INFORMATION FOR SEQ ID NO: 28 :  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: 1  
; IDENTIFICATION METHOD: by experiment  
; OTHER INFORMATION: Xaa in Location 1 represents N-(n-No. 5580956anoyl)-  
; OTHER INFORMATION: L-Leucine.  
; NAME/KEY: Modified-site  
; LOCATION: 11  
; IDENTIFICATION METHOD: by experiment  
; OTHER INFORMATION: Xaa in Location 11 represents L-Valine  
; OTHER INFORMATION: amide.  
US-08-146-152-28

Query Match 27.3%; Score 3; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KMR 10  
|||  
Db 4 KMR 6

RESULT 48

US-08-555-860-6

; Sequence 6, Application US/08555860

; Patent No. 5585474

; GENERAL INFORMATION:

; APPLICANT: IWAKI, Kanso

; APPLICANT: OHTA, Tsunetaka

; APPLICANT: KURIOTO, Masahi

; TITLE OF INVENTION: PROTEIN, DNA CODING SAID PROTEIN, AND

; TITLE OF INVENTION: PREPARATION OF SAID PROTEIN

; NUMBER OF SEQUENCES: 11

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BROWDY AND NEIMARK

; STREET: 419 Seventh Street, N.W., Suite 300

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20004

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/555,860

; FILING DATE: 13-NOV-1995

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/127,278

; FILING DATE: 27-SEP-1993

; APPLICATION NUMBER: JP 281136/1992

; FILING DATE: 28-SEP-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: NEIMARK, Sheridan

; REGISTRATION NUMBER: 20,520

; REFERENCE/DOCKET NUMBER: IWAKI=2

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-628-5197

; TELEFAX: 202-737-3528

; TELEX: 248633

; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-555-860-6



Query Match 27.3%; Score 3; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EGG 4  
|||  
Db 2 EGG 4

RESULT 49

US-08-347-000-4

; Sequence 4, Application US/08347000  
; Patent No. 5627265  
; GENERAL INFORMATION:  
; APPLICANT: Frazier, William A.  
; APPLICANT: Gao, Ai-Guo  
; TITLE OF INVENTION: Receptor for Cell-binding Domain of  
; TITLE OF INVENTION: Thrombospondins  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Scott J. Meyer, Monsanto/Searle, A3SG  
; STREET: 800 N. Lindbergh Blvd.  
; CITY: St. Louis  
; STATE: Missouri  
; COUNTRY: USA  
; ZIP: 63167  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/347,000  
; FILING DATE:  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/029,333  
; FILING DATE: 05-MAR-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meyer, Scott J.  
; REGISTRATION NUMBER: 25,275  
; REFERENCE/DOCKET NUMBER: WU-2848  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (314)694-3117  
; TELEFAX: (314)694-5435  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-347-000-4

Query Match 27.3%; Score 3; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GKK 6  
|||  
Db 9 GKK 11

RESULT 50

US-08-465-325-128

; Sequence 128, Application US/08465325

; Patent No. 5686563

; GENERAL INFORMATION:

; APPLICANT: Magainin Pharmaceuticals Inc.

; APPLICANT: 5110 Campus Drive

; APPLICANT: Plymouth Meeting, PA 19462

; TITLE OF INVENTION: Biologically Active Peptides Having

; TITLE OF INVENTION: N-Terminal Substitutions

; NUMBER OF SEQUENCES: 153

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &

; ADDRESSEE: Dunner

; STREET: 1300 I. Street, N.W. Suite 700

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20005-3315

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/465,325

; FILING DATE: 05-JUN-1995

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/184,462

; FILING DATE: 18-JAN-94

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/891,201

; FILING DATE: 01-JUN-92

; ATTORNEY/AGENT INFORMATION:

; NAME: Fordis, Jean B

; REGISTRATION NUMBER: 32,984

; REFERENCE/DOCKET NUMBER: 05387.0021-03000

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202) 408-4000

; TELEFAX: (202) 408-4400

; INFORMATION FOR SEQ ID NO: 128:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-465-325-128

Query Match

27.3%; Score 3; DB 1; Length 11;

Best Local Similarity 100.0%; Pred. No. 3.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KKK 7  
|||  
Db 1 KKK 3

RESULT 51

US-08-416-035-8

; Sequence 8, Application US/08416035

; Patent No. 5739278

; GENERAL INFORMATION:

; APPLICANT: Daum, Gunter

; APPLICANT: Cool, Deborah E.

; APPLICANT: Fischer, Edmond H.

; TITLE OF INVENTION: Methods and Compositions for Protein

; TITLE OF INVENTION: Tyrosine Phosphatases

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Seed and Berry

; STREET: 6300 Columbia Center, 701 Fifth Avenue

; CITY: Seattle

; STATE: Washington

; COUNTRY: USA

; ZIP: 98104

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/416,035

; FILING DATE: 30-MAR-1995

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/059,949

; FILING DATE: 10-MAY-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Sharkey, Richard G.

; REGISTRATION NUMBER: 32,629

; REFERENCE/DOCKET NUMBER: 940010.531

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (206) 622-4900

; TELEFAX: (206) 682-6031

; TELEX: 3723836

; INFORMATION FOR SEQ ID NO: 8:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-416-035-8

Query Match 27.3%; Score 3; DB 1; Length 11;

Best Local Similarity 100.0%; Pred. No. 3.4e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KKK 7  
|||  
Db 9 KKK 11

RESULT 52

US-08-082-269D-2

; Sequence 2, Application US/08082269D  
; Patent No. 5773227  
; GENERAL INFORMATION:  
; APPLICANT: Kuhn, Michael  
; APPLICANT: Meyer, Tobias  
; APPLICANT: Allbritton, Nancy  
; TITLE OF INVENTION: Bifunctional Chelating Polysaccharides  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Molecular Probes, Inc.  
; STREET: 4849 Pitchford Avenue  
; CITY: Eugene  
; STATE: Oregon  
; COUNTRY: USA  
; ZIP: 97402-9144  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.5 inch  
; COMPUTER: IBM  
; OPERATING SYSTEM: MS-DOS 6.2  
; SOFTWARE: Text Editor  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/082,269D  
; FILING DATE: 23-June-1993  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Helfenstein, Allegra J.  
; REGISTRATION NUMBER: 34,179  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (503)465-8300  
; TELEFAX: (503)344-6504  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 AMINO ACIDS  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
; MOLECULE TYPE: Peptide  
; HYPOTHETICAL: no  
; FRAGMENT TYPE:  
; PUBLICATION INFORMATION:  
; AUTHORS: Chelsky, Daniel, Ralph, Rebecca and Jonak, Gerald  
; TITLE: Sequence Requirements for Synthetic Peptide-Mediated  
Translocation to the  
; Patent No. 5773227  
; JOURNAL: Molecular and Cellular Biology  
; VOLUME: 9  
; ISSUE: 6  
; PAGES: 2487-2492  
; DATE: 1989  
US-08-082-269D-2

Query Match 27.3%; Score 3; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KKK 7  
|||  
Db 5 KKK 7

RESULT 53

US-08-408-604A-50

; Sequence 50, Application US/08408604A

; Patent No. 5801149

; GENERAL INFORMATION:

; APPLICANT: Shoelson, Steven

; TITLE OF INVENTION: INHIBITION OF SIGNAL TRANSDUCTION MOLECULES

; NUMBER OF SEQUENCES: 211

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LAHIVE & COCKFIELD

; STREET: 60 State Street, Suite 510

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02109-1875

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/408,604A

; FILING DATE: 21-MAR-1995

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/134,558

; FILING DATE: 08-OCT-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/959,949

; FILING DATE: 09-OCT-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/722,359

; FILING DATE: 19-JUNE-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Myers, Louis

; REGISTRATION NUMBER: 35,965

; REFERENCE/DOCKET NUMBER: JDP-014CP3

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617)227-7400

; TELEFAX: (617)227-5941

; INFORMATION FOR SEQ ID NO: 50:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; FRAGMENT TYPE: internal

US-08-408-604A-50

Query Match 27.3%; Score 3; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GGK 5  
|||  
Db 8 GGK 10

RESULT 54

US-08-511-662-5

; Sequence 5, Application US/08511662  
; Patent No. 5807552  
; GENERAL INFORMATION:  
; APPLICANT: Stanton, G. John  
; APPLICANT: Hughes, Jr., Thomas K.  
; APPLICANT: Smith, Eric M.  
; TITLE OF INVENTION: Compositions for Conferring Immunogenicity  
; TITLE OF INVENTION: to a Substance and Uses Thereof  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P.O. Box 4433  
; CITY: Houston  
; STATE: TX  
; COUNTRY: USA  
; ZIP: 77210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/511,662  
; FILING DATE: Concurrently herewith  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hodgins, Daniel S.  
; REGISTRATION NUMBER: 31,026  
; REFERENCE/DOCKET NUMBER: UTSG:162/HOD  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 515/418-3000  
; TELEFAX: 512/474-7577  
; TELEX: NA  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide

US-08-511-662-5

Query Match 27.3%; Score 3; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.4e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 MRA 11  
|||  
Db 9 MRA 11

RESULT 55

US-08-807-030-42

; Sequence 42, Application US/08807030

; Patent No. 5817755

; GENERAL INFORMATION:

; APPLICANT: Eyre, David R.

; APPLICANT: Clemens, J. Daniel

; APPLICANT: Ochs, Vincent W.

; TITLE OF INVENTION: Synthetic Peptide Analogs of NTx

; NUMBER OF SEQUENCES: 74

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Christensen O'Connor Johnson & Kindness

; ADDRESSEE: PLLC

; STREET: 1420 Fifth Avenue, Suite 2800

; CITY: Seattle

; STATE: Washington

; COUNTRY: U.S.A.

; ZIP: 98101

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/807,030

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/446,206

; FILING DATE: 19-MAY-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Shelton, Dennis K.

; REGISTRATION NUMBER: 26,997

; REFERENCE/DOCKET NUMBER: WROS110387

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 206 224 0718

; TELEFAX: 206 224 0779

; INFORMATION FOR SEQ ID NO: 42:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; FRAGMENT TYPE: N-terminal

; FEATURE:

; NAME/KEY: misc-feature

; LOCATION: 1

; OTHER INFORMATION: Xaa is pyroglutamic acid

US-08-807-030-42

Query Match 27.3%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GGK 5  
|||  
Db 8 GGK 10

RESULT 56

US-08-478-386A-59

; Sequence 59, Application US/08478386A  
; Patent No. 5830462  
; GENERAL INFORMATION:  
; APPLICANT: Crabtree, Gerald R.  
; APPLICANT: Schreiber, Stuart L.  
; APPLICANT: Spencer, David M.  
; APPLICANT: Wandless, Thomas J.  
; APPLICANT: Belshaw, Peter  
; TITLE OF INVENTION: REGULATED TRANSCRIPTION OF TARGETED  
; TITLE OF INVENTION: GENES AND OTHER BIOLOGICAL EVENTS  
; NUMBER OF SEQUENCES: 81  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ARIAD Pharmaceuticals, Inc.  
; STREET: 26 Landsdowne Street  
; CITY: Cambridge  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02139  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC/DOS/MS/DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/478,386A  
; FILING DATE: 07/JUN/1995  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Figg, E. Anthony  
; REGISTRATION NUMBER: 27,195  
; REFERENCE/DOCKET NUMBER: 2054-114A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 783-6040  
; TELEFAX: (202) 783-6031  
; INFORMATION FOR SEQ ID NO: 59:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: Peptide  
; LOCATION: 1..11  
; OTHER INFORMATION: /note= "Translation product of SEQ ID  
; OTHER INFORMATION: NOS:58 and 60."



US-08-478-386A-59

Query Match 27.3%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KKK 7  
|||  
Db 4 KKK 6

RESULT 57

US-08-292-597-59

; Sequence 59, Application US/08292597  
; Patent No. 5834266  
; GENERAL INFORMATION:  
; APPLICANT: Gerald R. Crabtree  
; APPLICANT: Schreiber, Stuart L.  
; APPLICANT: Spencer, David M.  
; APPLICANT: Wandless, Thomas J.  
; APPLICANT: Belshaw, Peter  
; TITLE OF INVENTION: Regulated Apoptosis  
; NUMBER OF SEQUENCES: 81  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ARIAD Pharmaceuticals, Inc.  
; STREET: 26 Landsdowne Street  
; CITY: Cambridge  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02139  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC/DOS/MS/DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/292,597  
; FILING DATE: 18/AUG/1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Figg, E. Anthony  
; REGISTRATION NUMBER: 27,195  
; REFERENCE/DOCKET NUMBER: 2054-108A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 783-6040  
; TELEFAX: (202) 783-6031  
; INFORMATION FOR SEQ ID NO: 59:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: Peptide

; LOCATION: 1..11  
; OTHER INFORMATION: /note= "Translation product of SEQ  
; OTHER INFORMATION: ID NOS:58 and 60."  
US-08-292-597-59

Query Match 27.3%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KKK 7  
|||  
Db 4 KKK 6

RESULT 58

US-08-719-758-3

; Sequence 3, Application US/08719758

; Patent No. 5837537

; GENERAL INFORMATION:

; APPLICANT: Campbell, Kevin P.

; APPLICANT: Jung, Daniel

; APPLICANT: Duclos, Franck

; APPLICANT: Straub, Volker

; TITLE OF INVENTION: k-SARCOGLYCAN NUCLEIC ACID SEQUENCES, AMINO

; TITLE OF INVENTION: ACID SEQUENCES AND APPLICATIONS

; NUMBER OF SEQUENCES: 21

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Kevin M. Farrell, P.C.

; STREET: P.O. Box 999

; CITY: York Harbor

; STATE: ME

; COUNTRY: USA

; ZIP: 03911

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/719,758

; FILING DATE:

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Farrell, Kevin M.

; REGISTRATION NUMBER: 35,505

; REFERENCE/DOCKET NUMBER: UIRF-9601

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (207) 363-0558

; TELEFAX: (207) 363-0528

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-719-758-3

Query Match 27.3%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEG 3  
|||  
Db 4 AEG 6

RESULT 59

US-08-244-496-29

; Sequence 29, Application US/08244496  
; Patent No. 5837686  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: PEPTIDES AND ANTIBODIES FOR TREATMENT OF  
; TITLE OF INVENTION: RHEUMATOID ARTHRITIS  
; NUMBER OF SEQUENCES: 85  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/244,496  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9125024.1  
; FILING DATE: 25-NOV-1991  
; INFORMATION FOR SEQ ID NO: 29:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: 11  
; OTHER INFORMATION: /product= "OTHER"  
; OTHER INFORMATION: /note= "AMIDATED"  
US-08-244-496-29

Query Match 27.3%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 G GK 5  
|||  
Db 9 G GK 11

RESULT 60

US-08-701-124-19

; Sequence 19, Application US/08701124  
; Patent No. 5846782  
; GENERAL INFORMATION:

```

; APPLICANT: Wickham, Thomas J.
; APPLICANT: Roelvink, Petrus W.
; APPLICANT: Kovesdi, Imre
; TITLE OF INVENTION: TARGETING ADENOVIRUS WITH USE OF
; TITLE OF INVENTION: CONSTRAINED PEPTIDE MOTIFS
; NUMBER OF SEQUENCES: 80
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Leydig, Voit & Mayer, Ltd.
;   STREET: Two Prudential Plaza - 49th Floor
;   CITY: Chicago
;   STATE: Illinois
;   COUNTRY: USA
;   ZIP: 60601
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/701,124
;   FILING DATE: 21-AUG-1996
; INFORMATION FOR SEQ ID NO: 19:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 11 amino acids
;     TYPE: amino acid
;     TOPOLOGY: linear
;   MOLECULE TYPE: peptide
US-08-701-124-19

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```

Query Match          27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches      3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      5 KKK 7
      |||
Db      3 KKK 5

```

# RESULT 61

US-08-621-803-206

```

; Sequence 206, Application US/08621803
; Patent No. 5851802

```

## GENERAL INFORMATION:

```

; APPLICANT: Better, Marc D.
; TITLE OF INVENTION: Methods for Recombinant Microbial Production of
; TITLE OF INVENTION: Fusion Proteins and BPI-Derived Peptides
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
;   STREET: 6300 Sears Tower, 233 South Wacker Drive
;   CITY: Chicago
;   STATE: Illinois
;   COUNTRY: United States of America
;   ZIP: 60606-6402
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible

```

```

;   OPERATING SYSTEM:  PC-DOS/MS-DOS
;   SOFTWARE:  PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  US/08/621,803
;   FILING DATE:  22-MAR-1996
;   ATTORNEY/AGENT INFORMATION:
;   NAME:  Borun, Michael F.
;   REGISTRATION NUMBER:  25,447
;   REFERENCE/DOCKET NUMBER:  27129/33199
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  312/474-6300
;   TELEFAX:  312/474-0448
;   TELEX:  25-3856
;   INFORMATION FOR SEQ ID NO:  206:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH:  11 amino acids
;   TYPE:  amino acid
;   TOPOLOGY:  linear
;   MOLECULE TYPE:  peptide
;   FEATURE:
;   NAME/KEY:  misc_feature
;   OTHER INFORMATION:  "XMP.350"
;   FEATURE:
;   NAME/KEY:  Modified-site
;   LOCATION:  C-Terminus
;   OTHER INFORMATION:  /label= Amidation
;   OTHER INFORMATION:  /note= "The C-Terminus is Amidated."
US-08-621-803-206

```

```

Query Match          27.3%;  Score 3;  DB 2;  Length 11;
Best Local Similarity 100.0%;  Pred. No. 3.4e+03;
Matches      3;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

```

```

Qy      5 KKK 7
      |||
Db      1 KKK 3

```

# RESULT 62

US-08-621-259A-181

```

; Sequence 181, Application US/08621259A
; Patent No. 5858974
; GENERAL INFORMATION:
;   APPLICANT:  Little II, Roger G
;   APPLICANT:  Lim, Edward
;   APPLICANT:  Fadem, Mitchell B.
;   TITLE OF INVENTION:  Anti-Fungal Peptides
;   NUMBER OF SEQUENCES:  252
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE:  McAndrews, Held & Malloy, Ltd.
;   STREET:  500 West Madison Street
;   CITY:  Chicago
;   STATE:  Illinois
;   COUNTRY:  United States of America
;   ZIP:  60661
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE:  Floppy disk

```

```

;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;      CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/621,259A
;      FILING DATE:  21-MAR-1996
;      PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/504,841
;      FILING DATE:  20-JUL-1995
;      ATTORNEY/AGENT INFORMATION:
;      NAME:  McNicholas, Janet M.
;      REGISTRATION NUMBER:  32,918
;      REFERENCE/DOCKET NUMBER:  11021US02
;      TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/707-8889
;      TELEFAX:  312/707-9155
;      TELEX:
;      INFORMATION FOR SEQ ID NO:  181:
;      SEQUENCE CHARACTERISTICS:
;      LENGTH:  11 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;      MOLECULE TYPE:  peptide
;      FEATURE:
;      NAME/KEY:  misc_feature
;      OTHER INFORMATION:  "XMP.350"
;      FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  C-Terminus
;      OTHER INFORMATION:  /label= Amidation
;      OTHER INFORMATION:  /note= "The C-Terminus is Amidated."
US-08-621-259A-181

```

```

Query Match          27.3%;  Score 3;  DB 2;  Length 11;
Best Local Similarity 100.0%;  Pred. No. 3.4e+03;
Matches      3;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

```

```

Qy      5 KKK 7
      |||
Db      1 KKK 3

```

# RESULT 63

US-08-388-653-59

```

; Sequence 59, Application US/08388653
; Patent No. 5869337
; GENERAL INFORMATION:
; APPLICANT:  Crabtree, Gerald R.
; APPLICANT:  Schreiber, Stuart L.
; APPLICANT:  Spencer, David M.
; APPLICANT:  Wandless, Thomas J.
; APPLICANT:  Belshaw, Peter
; TITLE OF INVENTION:  REGULATED TRANSCRIPTION OF TARGETED
; TITLE OF INVENTION:  GENES AND OTHER BIOLOGICAL EVENTS
; NUMBER OF SEQUENCES:  81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE:  ARIAD Pharmaceuticals, Inc.

```

```

; STREET: 26 Landsdowne Street
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02139
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC/DOS/MS/DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,653
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/478,386
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Figg, E. Anthony
; REGISTRATION NUMBER: 27,195
; REFERENCE/DOCKET NUMBER: 2054-114A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 783-6040
; TELEFAX: (202) 783-6031
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..11
; OTHER INFORMATION: /note= "Translation product of SEQ ID
; OTHER INFORMATION: NOS:58 and 60."

```

US-08-388-653-59

```

Query Match          27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      5 KKK 7
        |||
Db      4 KKK 6

```

RESULT 64

US-08-473-985-59

```

; Sequence 59, Application US/08473985
; Patent No. 5871753
; GENERAL INFORMATION:
; APPLICANT: Crabtree, Gerald R.
; APPLICANT: Schreiber, Stuart L.
; APPLICANT: Spencer, David M.
; APPLICANT: Wandless, Thomas J.
; APPLICANT: Belshaw, Peter
; APPLICANT: Ho, Steffan

```

```

; TITLE OF INVENTION: Regulated Transcription of Targeted Genes and
; TITLE OF INVENTION: Other Biological Events
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/473,985
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/179,748
; FILING DATE: 07-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-SU 9863
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..11
; OTHER INFORMATION: /note= "Translation product of SEQ
; OTHER INFORMATION: ID NOS:58 and 60."
US-08-473-985-59

```

```

Query Match          27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      5 KKK 7
      |||
Db      4 KKK 6

```

```

RESULT 65
US-08-938-367-1
; Sequence 1, Application US/08938367
; Patent No. 5955582
; GENERAL INFORMATION:
; APPLICANT: Newman, Karel

```



```

; APPLICANT: Ogbonna, Godwin
; APPLICANT: Odegaard, Bruce
; APPLICANT: Schmidt, Jane
; TITLE OF INVENTION: AN ANTIBODY AGAINST A 3-A
; TITLE OF INVENTION: MINOPHENYLBORONIC-GLYCATED PROTEIN COMPLEX
; TITLE OF INVENTION: AND ITS USE IN AN IMMUNOASSAY
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Beckman Coulter, Inc.
; STREET: 4300 N. Harbor Blvd, P.O. Box 3100
; CITY: Fullerton
; STATE: CA
; COUNTRY: USA
; ZIP: 92834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSEQ for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/938,367
; FILING DATE: 26-SEP-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: May, William H
; REGISTRATION NUMBER: 26,769
; REFERENCE/DOCKET NUMBER: 174D-1726
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 714-871-4848
; TELEFAX: 714-773-7936
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-938-367-1

```

```

Query Match          27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      2 EGG 4
        |||
Db      6 EGG 8

```

```

RESULT 66
US-08-053-451B-159
; Sequence 159, Application US/08053451B
; Patent No. 5955584
; GENERAL INFORMATION:

```

; APPLICANT: Chen, Francis W.  
 ; APPLICANT: Ditlow, Charles C.  
 ; APPLICANT: Calenoff, Emanuel  
 ; TITLE OF INVENTION: ATHEROSCLEROTIC PLAQUE SPECIFIC  
 ; TITLE OF INVENTION: ANTIGENS, ANTIBODIES THERETO, AND USES THEREOF  
 ; NUMBER OF SEQUENCES: 176  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Pennie & Edmonds  
 ; STREET: 1155 Avenue of the Americas  
 ; CITY: New York  
 ; STATE: New York  
 ; COUNTRY: USA  
 ; ZIP: 10036  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/053,451B  
 ; FILING DATE: 26-APR-1993  
 ; CLASSIFICATION: 424  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Halluin, Albert P.  
 ; REGISTRATION NUMBER: 25,227  
 ; REFERENCE/DOCKET NUMBER: 7606-033-999  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 415-854-3660  
 ; TELEFAX: 415-854-3694  
 ; TELEX: 66141 PENNIE  
 ; INFORMATION FOR SEQ ID NO: 159:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 11 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: unknown  
 ; TOPOLOGY: unknown  
 ; MOLECULE TYPE: protein  
 US-08-053-451B-159

Query Match 27.3%; Score 3; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 3.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 MRA 11  
 |||  
 Db 1 MRA 3

RESULT 67  
 US-08-483-898-59  
 ; Sequence 59, Application US/08483898  
 ; Patent No. 5994313  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gerald R. Crabtree  
 ; APPLICANT: Schreiber, Stuart L.  
 ; APPLICANT: Spencer, David M.  
 ; APPLICANT: Wandless, Thomas J.

```

; APPLICANT: Belshaw, Peter
; TITLE OF INVENTION: Regulated Apoptosis
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARIAD Pharmaceuticals, Inc.
; STREET: 26 Landsdowne Street
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02139
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC/DOS/MS/DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,898
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/292,597
; FILING DATE: 18-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Figg, E. Anthony
; REGISTRATION NUMBER: 27,195
; REFERENCE/DOCKET NUMBER: 2054-108A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 783-6040
; TELEFAX: (202) 783-6031
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..11
; OTHER INFORMATION: /note= "Translation product of SEQ
; OTHER INFORMATION: ID NOS:58 and 60."
US-08-483-898-59

```

```

Query Match          27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      5 KKK 7
      |||
Db      4 KKK 6

```

```

RESULT 68
US-08-369-643-75
; Sequence 75, Application US/08369643A
; Patent No. 6004757
; GENERAL INFORMATION:
; APPLICANT: Cantley, Lewis C.

```

```
; APPLICANT: Songyang, Zhou
; TITLE OF INVENTION: Substrate Specificity of Protein Kinases
; FILE REFERENCE: CNS-001CP
; CURRENT APPLICATION NUMBER: US/08/369,643A
; CURRENT FILING DATE: 1995-01-06
; EARLIER APPLICATION NUMBER: US 08/178,570
; EARLIER FILING DATE: 1994-01-07
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 75
;   LENGTH: 11
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:peptide
;   OTHER INFORMATION: synthesized as a substrate for cyclin containing
;   OTHER INFORMATION: kinases
US-08-369-643-75
```

```
Query Match          27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;
```

```
Qy      5 KKK 7
        |||
Db      8 KKK 10
```

# RESULT 69

US-08-750-419A-29

```
; Sequence 29, Application US/08750419A
; Patent No. 6008340
; GENERAL INFORMATION:
;   APPLICANT: BALL, TANJA
;   APPLICANT: VRTALA, SUSANNE
;   APPLICANT: SPERR, WOLFGANG
;   APPLICANT: VALENT, PETER
;   APPLICANT: SUSANI, MARKUS
;   APPLICANT: KRAFT, DIETRICH
;   APPLICANT: LAFFER, SYLVIA
;   TITLE OF INVENTION: RECOMBINANT ALLERGEN, FRAGMENTS THEREOF,
;   TITLE OF INVENTION: CORRESPONDING RECOMBINANT DNA MOLECULES, VECTORS AND
HOSTS
;   TITLE OF INVENTION: CONTAINING THE DNA MOLECULES, DIAGNOSTIC AND
THERAPEUTIC
;   TITLE OF INVENTION: USES OF SAID ALLERGENS AND FRAGMENTS
;   NUMBER OF SEQUENCES: 33
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
;   STREET: PO BOX 747
;   CITY: FALLS CHURCH
;   STATE: VA
;   COUNTRY: USA
;   ZIP: 22040-0747
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
```

```

;   OPERATING SYSTEM:  PC-DOS/MS-DOS
;   SOFTWARE:  PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  US/08/750,419A
;   FILING DATE:
;   CLASSIFICATION:  536
;   ATTORNEY/AGENT INFORMATION:
;   NAME:  MURPHY JR, GERALD M
;   REGISTRATION NUMBER:  28,977
;   REFERENCE/DOCKET NUMBER:  1614-175
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  (703) 205-8000
;   TELEFAX:  (703) 205-8050
;   INFORMATION FOR SEQ ID NO:  29:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH:  11 amino acids
;   TYPE:  amino acid
;   STRANDEDNESS:  not relevant
;   TOPOLOGY:  linear
;   MOLECULE TYPE:  peptide
US-08-750-419A-29

```

```

Query Match          27.3%;  Score 3;  DB 3;  Length 11;
Best Local Similarity 100.0%;  Pred. No. 3.4e+03;
Matches      3;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

```

```

Qy      2 EGG 4
      |||
Db      5 EGG 7

```

# RESULT 70

US-09-087-716-59

```

; Sequence 59, Application US/09087716
; Patent No. 6011018
;   GENERAL INFORMATION:
;   APPLICANT:  Crabtree, Gerald R.
;   APPLICANT:  Schreiber, Stuart L.
;   APPLICANT:  Spencer, David M.
;   APPLICANT:  Wandless, Thomas J.
;   APPLICANT:  Belshaw, Peter
;   TITLE OF INVENTION:  REGULATED TRANSCRIPTION OF TARGETED
;   TITLE OF INVENTION:  GENES AND OTHER BIOLOGICAL EVENTS
;   NUMBER OF SEQUENCES:  81
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE:  ARIAD Pharmaceuticals, Inc.
;   STREET:  26 Landsdowne Street
;   CITY:  Cambridge
;   STATE:  Massachusetts
;   COUNTRY:  USA
;   ZIP:  02139
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE:  Floppy disk
;   COMPUTER:  IBM PC compatible
;   OPERATING SYSTEM:  PC/DOS/MS/DOS
;   SOFTWARE:  PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:

```

```

; APPLICATION NUMBER: US/09/087,716
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/388,653
; FILING DATE: 02/14/1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Figg, E. Anthony
; REGISTRATION NUMBER: 27,195
; REFERENCE/DOCKET NUMBER: 2054-114A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 783-6040
; TELEFAX: (202) 783-6031
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..11
; OTHER INFORMATION: /note= "Translation product of SEQ ID
; OTHER INFORMATION: NOS:58 and 60."
US-09-087-716-59

```

```

Query Match          27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      5 KKK 7
      |||
Db      4 KKK 6

```

# RESULT 71

US-09-015-003-5

```

; Sequence 5, Application US/09015003
; Patent No. 6030783
; GENERAL INFORMATION:
; APPLICANT: KANE, Stefanie A.
; APPLICANT: LIPPARD, Stephen J.
; TITLE OF INVENTION: Photo-Potentiation of Cisplatin
; TITLE OF INVENTION: Chemotherapy
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patent Administrator, Testa, Hurwitz &
; ADDRESSEE: Thibeault, LLP
; STREET: 125 High St.
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

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;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/015,003
;   FILING DATE:
;   CLASSIFICATION:
;   ATTORNEY/AGENT INFORMATION:
;   NAME: FENTON, Gillian M.
;   REGISTRATION NUMBER: 36,508
;   REFERENCE/DOCKET NUMBER: MIT-079
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (617) 248-7000
;   TELEFAX: (617) 248-7100
;   INFORMATION FOR SEQ ID NO: 5:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 11 amino acids
;   TYPE: amino acid
;   STRANDEDNESS:
;   TOPOLOGY: linear
;   MOLECULE TYPE: peptide
US-09-015-003-5

```

```

Query Match          27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      5 KKK 7
      |||
Db      2 KKK 4

```

# RESULT 72

US-09-157-753-59

```

; Sequence 59, Application US/09157753
; Patent No. 6043082
; GENERAL INFORMATION:
;   APPLICANT: Crabtree, Gerald R.
;   APPLICANT: Schreiber, Stuart L.
;   APPLICANT: Spencer, David M.
;   APPLICANT: Wandless, Thomas J.
;   APPLICANT: Belshaw, Peter
;   TITLE OF INVENTION: REGULATED TRANSCRIPTION OF TARGETED
;   TITLE OF INVENTION: GENES AND OTHER BIOLOGICAL EVENTS
;   NUMBER OF SEQUENCES: 81
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: ARIAD Pharmaceuticals, Inc.
;   STREET: 26 Landsdowne Street
;   CITY: Cambridge
;   STATE: Massachusetts
;   COUNTRY: USA
;   ZIP: 02139
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC/DOS/MS/DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/157,753

```

```

; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/388,653
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: US 08/478,386
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Figg, E. Anthony
; REGISTRATION NUMBER: 27,195
; REFERENCE/DOCKET NUMBER: 2054-114A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 783-6040
; TELEFAX: (202) 783-6031
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..11
; OTHER INFORMATION: /note= "Translation product of SEQ ID
; OTHER INFORMATION: NOS:58 and 60."
US-09-157-753-59

```

```

Query Match          27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      5 KKK 7
        |||
Db      4 KKK 6

```

# RESULT 73

US-09-157-230-59

```

; Sequence 59, Application US/09157230
; Patent No. 6046047
; GENERAL INFORMATION:
; APPLICANT: Crabtree, Gerald R.
; APPLICANT: Schreiber, Stuart L.
; APPLICANT: Spencer, David M.
; APPLICANT: Wandless, Thomas J.
; APPLICANT: Belshaw, Peter
; TITLE OF INVENTION: REGULATED TRANSCRIPTION OF TARGETED
; TITLE OF INVENTION: GENES AND OTHER BIOLOGICAL EVENTS
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARIAD Pharmaceuticals, Inc.
; STREET: 26 Landsdowne Street
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02139
; COMPUTER READABLE FORM:

```



```

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC/DOS/MS/DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/157,230
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/478,386
; FILING DATE: 07/JUN/1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Figg, E. Anthony
; REGISTRATION NUMBER: 27,195
; REFERENCE/DOCKET NUMBER: 2054-114A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 783-6040
; TELEFAX: (202) 783-6031
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..11
; OTHER INFORMATION: /note= "Translation product of SEQ ID
; OTHER INFORMATION: NOS:58 and 60."
US-09-157-230-59

```

```

Query Match          27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      5 KKK 7
      |||
Db      4 KKK 6

```

# RESULT 74

US-09-087-811-59

```

; Sequence 59, Application US/09087811
; Patent No. 6054436
; GENERAL INFORMATION:
; APPLICANT: Gerald R. Crabtree
; APPLICANT: Schreiber, Stuart L.
; APPLICANT: Spencer, David M.
; APPLICANT: Wandless, Thomas J.
; APPLICANT: Belshaw, Peter
; TITLE OF INVENTION: Regulated Apoptosis
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARIAD Pharmaceuticals, Inc.
; STREET: 26 Landsdowne Street
; CITY: Cambridge
; STATE: Massachusetts

```

```

; COUNTRY: USA
; ZIP: 02139
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC/DOS/MS/DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/087,811
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/292,597
; FILING DATE: 18-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Figg, E. Anthony
; REGISTRATION NUMBER: 27,195
; REFERENCE/DOCKET NUMBER: 2054-108A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 783-6040
; TELEFAX: (202) 783-6031
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..11
; OTHER INFORMATION: /note= "Translation product of SEQ
; OTHER INFORMATION: ID NOS:58 and 60."
US-09-087-811-59

```

```

Query Match          27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      5 KKK 7
        |||
Db      4 KKK 6

```

RESULT 75

US-09-130-225-19

```

; Sequence 19, Application US/09130225
; Patent No. 6057155
; GENERAL INFORMATION:
; APPLICANT: Wickham, Thomas J.
; APPLICANT: Roelvink, Petrus W.
; APPLICANT: Kovesdi, Imre
; TITLE OF INVENTION: TARGETING ADENOVIRUS WITH USE OF
; TITLE OF INVENTION: CONSTRAINED PEPTIDE MOTIFS
; NUMBER OF SEQUENCES: 80
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leydig, Voit & Mayer, Ltd.
; STREET: Two Prudential Plaza - 49th Floor

```

; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60601  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/130,225  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 8-701124  
; FILING DATE: 21-AUG-1996  
; INFORMATION FOR SEQ ID NO: 19:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-09-130-225-19

Query Match 27.3%; Score 3; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KKK 7  
|||  
Db 3 KKK 5

Search completed: April 8, 2004, 15:52:14  
Job time : 12.3077 secs

OM protein - protein search, using sw model

Run on: April 8, 2004, 15:30:07 ; Search time 8.61538 Seconds  
(without alignments)  
122.816 Million cell updates/sec

Title: US-09-787-443A-19  
Perfect score: 11  
Sequence: 1 AEGGKKKKMRA 11

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 283366 seqs, 96191526 residues

Word size : 0

Total number of hits satisfying chosen parameters: 226

Minimum DB seq length: 11

Maximum DB seq length: 11

Post-processing: Listing first 100 summaries

Database : PIR\_78:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	%		DB	ID	Description
		Query	Match Length			
1	3	27.3	11	2	PU0029	33K protein 3218 -
2	3	27.3	11	2	PC2173	triacylglycerol li
3	3	27.3	11	2	S57575	T cell receptor V-
4	3	27.3	11	2	S60294	tubulin 2 beta-3 c
5	2	18.2	11	1	GMROL	leucosulfakinin -
6	2	18.2	11	2	S66196	alcohol dehydrogen
7	2	18.2	11	2	A33917	dihydroorotase (EC
8	2	18.2	11	2	PQ0682	photosystem I 17.5
9	2	18.2	11	2	C53652	rhlR protein - Pse
10	2	18.2	11	2	YHRT	morphogenetic neur
11	2	18.2	11	2	YHHU	morphogenetic neur
12	2	18.2	11	2	YHBO	morphogenetic neur
13	2	18.2	11	2	YHXAE	morphogenetic neur

14	2	18.2	11	2	YHJFHY	morphogenetic neur
15	2	18.2	11	2	S42449	ant1 protein - pha
16	2	18.2	11	2	C58501	42K bile stone pro
17	2	18.2	11	2	JQ0395	hypothetical prote
18	2	18.2	11	2	PQ0231	beta-glucosidase (
19	2	18.2	11	2	S66606	quinoline 2-oxidor
20	2	18.2	11	2	S58244	pyrroloquinoline q
21	2	18.2	11	2	S04875	nifS protein - Bra
22	2	18.2	11	2	E60691	phycobilisome 8K l
23	2	18.2	11	2	S33519	probable secreted
24	2	18.2	11	2	T06383	hypothetical prote
25	2	18.2	11	2	S19775	wound-induced prot
26	2	18.2	11	2	S41747	chaperonin 10 homo
27	2	18.2	11	2	A38590	transforming prote
28	2	18.2	11	2	A61512	variant surface gl
29	2	18.2	11	2	A35594	buccalin - Califor
30	2	18.2	11	2	A60656	perisulfakinin - A
31	2	18.2	11	2	S65395	chemical-sense-rel
32	2	18.2	11	2	I41978	calliFMRFamide 9 -
33	2	18.2	11	2	D37196	bradykinin-potenti
34	2	18.2	11	2	I65231	CCK-B gastrin rece
35	2	18.2	11	2	PT0249	Ig heavy chain CRD
36	2	18.2	11	2	PT0302	Ig heavy chain CRD
37	2	18.2	11	2	PH1343	Ig heavy chain DJ
38	2	18.2	11	2	S51732	T-cell receptor al
39	2	18.2	11	2	S60354	retinal oxidase -
40	2	18.2	11	2	PN0044	protein kinase C i
41	2	18.2	11	2	PT0209	T-cell receptor al
42	2	18.2	11	2	PT0218	T-cell receptor be
43	2	18.2	11	2	I41946	T-cell receptor ga
44	2	18.2	11	2	C49037	TcR gamma V-J regi
45	2	18.2	11	2	PD0441	translation elonga
46	2	18.2	11	2	I77447	urinary protein -
47	2	18.2	11	2	S65377	cytochrome-c oxida
48	2	18.2	11	2	S78422	ribosomal protein
49	2	18.2	11	2	PH0947	T-cell receptor be
50	2	18.2	11	2	I52304	gene rSSTR4 protei
51	2	18.2	11	2	A34243	H-hyosophorin - Ja
52	2	18.2	11	2	A61575	Trimeresurus serin
53	2	18.2	11	4	S19015	hypothetical prote
54	2	18.2	11	4	I54081	retinoic acid rece
55	1	9.1	11	1	XAVIBH	bradykinin-potenti
56	1	9.1	11	1	XASNBA	bradykinin-potenti
57	1	9.1	11	1	ECLQ2M	tachykinin II - mi
58	1	9.1	11	1	SPHO	substance P - hors
59	1	9.1	11	1	EOOCC	eledoisin - curled
60	1	9.1	11	1	A60654	substance P - quin
61	1	9.1	11	1	EOOC	eledoisin - musky
62	1	9.1	11	1	LFTWWE	probable trpEG lea
63	1	9.1	11	2	G42762	proteasome endopep
64	1	9.1	11	2	S68392	H+-transporting tw
65	1	9.1	11	2	B49164	chromogranin-B - r
66	1	9.1	11	2	JN0023	substance P - chic
67	1	9.1	11	2	S32575	ribosomal protein
68	1	9.1	11	2	A40693	transgelin - sheep
69	1	9.1	11	2	A38841	rhodopsin homolog
70	1	9.1	11	2	S00616	parasporal crystal

71	1	9.1	11	2	S09074	cytochrome P450-4b
72	1	9.1	11	2	A57458	gene Gax protein -
73	1	9.1	11	2	A26930	ermG leader peptid
74	1	9.1	11	2	D60409	kassinin-like pept
75	1	9.1	11	2	F60409	substance P-like p
76	1	9.1	11	2	E60409	substance P-like p
77	1	9.1	11	2	A61365	phyllokinin - Rohd
78	1	9.1	11	2	B26744	megascoliakinin -
79	1	9.1	11	2	S23308	substance P - rain
80	1	9.1	11	2	S23306	substance P - Atla
81	1	9.1	11	2	B60409	kassinin-like pept
82	1	9.1	11	2	C60409	kassinin-like pept
83	1	9.1	11	2	S07203	uperolein - frog (
84	1	9.1	11	2	S07207	Crinia-angiotensin
85	1	9.1	11	2	S07201	physalaemin - frog
86	1	9.1	11	2	A61033	ranatachykinin A -
87	1	9.1	11	2	D61033	ranatachykinin D -
88	1	9.1	11	2	B58501	24K kidney and bla
89	1	9.1	11	2	D58502	27K bile and gallb
90	1	9.1	11	2	A58502	38K kidney stone p
91	1	9.1	11	2	F58501	43.5K bile stone p
92	1	9.1	11	2	I41138	acetyl ornithine d
93	1	9.1	11	2	S42587	celF protein - Esc
94	1	9.1	11	2	S35490	type II site-speci
95	1	9.1	11	2	S21127	precorrin methyltr
96	1	9.1	11	2	S70720	trigger factor hom
97	1	9.1	11	2	S33782	acetolactate synth
98	1	9.1	11	2	B39853	LuxC protein - Pho
99	1	9.1	11	2	A58838	hemolysin - Porphy
100	1	9.1	11	2	B43669	hypothetical prote

#### ALIGNMENTS

##### RESULT 1

PU0029

33K protein 3218 - rice (strain Nohonbare) (fragment)

C;Species: Oryza sativa (rice)

C;Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 11-Apr-1995

C;Accession: PU0029

R;Tsugita, A.; Miyatake, N.

submitted to JIPID, April 1993

A;Reference number: PS0208

A;Accession: PU0029

A;Molecule type: protein

A;Residues: 1-11 <TSU>

A;Experimental source: bran

C;Comment: molecular weight 33K, pI 6.0.

Query Match 27.3%; Score 3; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 4e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EGG 4

|||

Db 3 EGG 5

RESULT 2

PC2173

triacylglycerol lipase (EC 3.1.1.3) II - *Rhizopus niveus* (strain IFO 4759)  
(fragments)

C;Species: *Rhizopus niveus*

C;Date: 03-May-1994 #sequence\_revision 07-Oct-1994 #text\_change 07-May-1999

C;Accession: PC2173

R;Kohno, M.; Kugimiya, W.; Hashimoto, Y.; Morita, Y.

Biosci. Biotechnol. Biochem. 58, 1007-1012, 1994

A;Title: Purification, characterization, and crystallization of two types of  
lipase from *Rhizopus niveus*.

A;Reference number: PC2171; MUID:94319059; PMID:7765029

A;Accession: PC2173

A;Molecule type: protein

A;Residues: 1-10;11 <KOH>

C;Comment: This enzyme catalyzes the hydrolysis of the ester bonds of  
triacylglycerols and the synthesis of ester bonds via transesterification.

C;Comment: This enzyme is produced from lipase I by limited proteolysis due to  
the action of a serine protease.

C;Keywords: carboxylic ester hydrolase

Query Match 27.3%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GGK 5

|||

Db 3 GGK 5

RESULT 3

S57575

T cell receptor V-J junctional alpha chain region - human (fragment)

C;Species: *Homo sapiens* (man)

C;Date: 19-Oct-1995 #sequence\_revision 17-Nov-1995 #text\_change 05-Nov-1999

C;Accession: S57575

R;Burrows, S.R.; Silins, S.L.; Moss, D.J.; Khanna, R.; Misko, I.S.; Argat, V.P.  
submitted to the EMBL Data Library, June 1995

A;Description: T cell receptor repertoire for a viral epitope in humans is  
diversified by tolerance to a background MHC antigen.

A;Reference number: S57494

A;Accession: S57575

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-11 <BUR>

A;Cross-references: EMBL:Z49953; NID:g887510; PIDN:CAA90224.1; PID:g887511

C;Keywords: T-cell receptor

Query Match 27.3%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GGK 5

|||

Db 5 GGK 7

RESULT 4

S60294

tubulin 2 beta-3 chain - fruit fly (*Drosophila melanogaster*) (fragment)

C;Species: *Drosophila melanogaster*

C;Date: 19-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 21-Jun-2002

C;Accession: S60294

R;Chapel, S.; Sobrier, M.L.; Montpied, P.; Micard, D.; Bruhat, A.; Couderc, J.L.; Dastugue, B.

Insect Mol. Biol. 2, 39-48, 1993

A;Title: In *Drosophila* Kc cells 20-OHE induction of the 60C beta-3 tubulin gene expression is a primary transcriptional event.

A;Reference number: S60292; MUID:97242543; PMID:9087542

A;Accession: S60294

A;Molecule type: mRNA

A;Residues: 1-11 <CHA>

A;Cross-references: EMBL:X60393

C;Genetics:

A;Gene: FlyBase:beta-Tub60D

A;Cross-references: FlyBase:FBgn0003888

Query Match 27.3%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GGK 5  
|||  
Db 9 GGK 11

RESULT 5

GMROL

leucosulfakinin - Madeira cockroach

N;Alternate names: LSK

C;Species: *Leucophaea maderae* (Madeira cockroach)

C;Date: 17-Mar-1987 #sequence\_revision 17-Mar-1987 #text\_change 13-Sep-1996

C;Accession: A01622

R;Nachman, R.J.; Holman, G.M.; Haddon, W.F.; Ling, N.

Science 234, 71-73, 1986

A;Title: Leucosulfakinin, a sulfated insect neuropeptide with homology to gastrin and cholecystokinin.

A;Reference number: A01622; MUID:86315858; PMID:3749893

A;Accession: A01622

A;Molecule type: protein

A;Residues: 1-11 <NAC>

C;Superfamily: gastrin

C;Keywords: amidated carboxyl end; hormone; sulfoprotein

F;6/Binding site: sulfate (Tyr) (covalent) #status experimental

F;11/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 18.2%; Score 2; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.4e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 MR 10  
||



Db

9 MR 10

RESULT 6

S66196

alcohol dehydrogenase (EC 1.1.1.1) class III high affinity form - cod (Gadus sp.) (fragment)

C;Species: Gadus sp. (cod)

C;Date: 14-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 12-Jun-1998

C;Accession: S66196

R;Hjelmqvist, L.; Hackett, M.; Shafqat, J.; Danielsson, O.; Iida, J.; Hendrickson, R.C.; Michel, H.; Shabanowitz, J.; Hunt, D.F.; Joernvall, H. FEBS Lett. 367, 237-240, 1995

A;Title: Multiplicity of N-terminal structures of medium-chain alcohol dehydrogenases. Mass-spectrometric analysis of plant, lower vertebrate and higher vertebrate class I, II, and III forms of the enzyme.

A;Reference number: S66191; MUID:95331382; PMID:7607314

A;Accession: S66196

A;Molecule type: protein

A;Residues: 1-11 <HJE>

C;Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology

C;Keywords: alcohol metabolism; NAD; oxidoreductase

Query Match 18.2%; Score 2; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 3.4e+04;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 RA 11

||

Db 5 RA 6

RESULT 7

A33917

dihydroorotase (EC 3.5.2.3) - Chinese hamster (fragment)

C;Species: Cricetulus griseus (Chinese hamster)

C;Date: 09-Mar-1990 #sequence\_revision 09-Mar-1990 #text\_change 07-Nov-1997

C;Accession: A33917

R;Simmer, J.P.; Kelly, R.E.; Scully, J.L.; Grayson, D.R.; Rinker Jr., A.G.; Bergh, S.T.; Evans, D.R.

Proc. Natl. Acad. Sci. U.S.A. 86, 4382-4386, 1989

A;Title: Mammalian aspartate transcarbamylase (ATCase): sequence of the ATCase domain and interdomain linker in the CAD multifunctional polypeptide and properties of the isolated domain.

A;Reference number: A33917; MUID:89282776; PMID:2543974

A;Accession: A33917

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-11 <SIM>

A;Cross-references: GB:M23652

C;Superfamily: rudimentary enzyme; aspartate/ornithine carbamoyltransferase homology; Bacillus dihydroorotase homology; biotin carboxylase homology; carbamoyl-phosphate synthase (ammonia) homology; carbamoyl-phosphate synthase (glutamine-hydrolyzing) large chain homology; carbamoyl-phosphate synthase (glutamine-hydrolyzing) small chain homology; trpG homology

C;Keywords: hydrolase

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.4e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EG 3  
||  
Db 2 EG 3

RESULT 8

PQ0682

photosystem I 17.5K D2 chain - common tobacco (fragment)

C;Species: *Nicotiana tabacum* (common tobacco)

C;Date: 19-May-1994 #sequence\_revision 19-May-1994 #text\_change 17-Mar-1999

C;Accession: PQ0682

R;Obokata, J.; Mikami, K.; Hayashida, N.; Nakamura, M.; Sugiura, M.

Plant Physiol. 102, 1259-1267, 1993

A;Title: Molecular heterogeneity of photosystem I. psaD, psaE, psaF, psaH and psaL are all present in isoforms in *Nicotiana* spp.

A;Reference number: PQ0667; MUID:94105345; PMID:8278548

A;Accession: PQ0682

A;Molecule type: protein

A;Residues: 1-11 <OBO>

C;Superfamily: photosystem I chain II

C;Keywords: chloroplast; photosynthesis; photosystem I; thylakoid

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.4e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AE 2  
||  
Db 1 AE 2

RESULT 9

C53652

rhlR protein - *Pseudomonas aeruginosa* (fragment)

C;Species: *Pseudomonas aeruginosa*

C;Date: 21-Jul-1995 #sequence\_revision 28-Jul-1995 #text\_change 21-Aug-1998

C;Accession: C53652

R;Ochsner, U.A.; Fiechter, A.; Reiser, J.

J. Biol. Chem. 269, 19787-19795, 1994

A;Title: Isolation, characterization, and expression in *Escherichia coli* of the *Pseudomonas aeruginosa* rhlAB genes encoding a rhamnosyltransferase involved in rhamnolipid biosurfactant synthesis.

A;Reference number: A53652; MUID:94327521; PMID:8051059

A;Accession: C53652

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-11 <OCH>

A;Cross-references: GB:L28170

C;Superfamily: sdiA regulatory protein

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.4e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy            3 GG 4  
              ||  
Db            5 GG 6

RESULT 10

YHRT

morphogenetic neuropeptide - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 20-Jun-2000 #sequence\_revision 20-Jun-2000 #text\_change 20-Jun-2000

C;Accession: A01427

R;Bodenmuller, H.; Schaller, H.C.

Nature 293, 579-580, 1981

A;Title: Conserved amino acid sequence of a neuropeptide, the head activator, from coelenterates to humans.

A;Reference number: A93266; MUID:82035850; PMID:7290191

A;Accession: A01427

A;Molecule type: protein

A;Residues: 1-11 <BOD>

R;Birrr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.

FEBS Lett. 131, 317-321, 1981

A;Title: Synthesis of a new neuropeptide, the head activator from hydra.

A;Reference number: A91296; MUID:82050803; PMID:7297679

A;Contents: annotation; synthesis

A;Note: the synthetic peptide was identical with the natural peptide in chemical structure and biological activity

C;Comment: This peptide was first isolated from nerve cells of hydra and was called head activator by the authors, because it induced head-specific growth and differentiation in this animal. It has been found in mammalian intestine and hypothalamus.

C;Superfamily: unassigned animal peptides

C;Keywords: growth factor; hormone; hypothalamus; intestine; neuropeptide; pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match                    18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity    100.0%; Pred. No. 3.4e+04;  
Matches        2; Conservative        0; Mismatches        0; Indels        0; Gaps        0;

Qy            3 GG 4  
              ||  
Db            4 GG 5

RESULT 11

YHHU

morphogenetic neuropeptide - human

C;Species: Homo sapiens (man)

C;Date: 20-Jun-2000 #sequence\_revision 20-Jun-2000 #text\_change 20-Jun-2000

C;Accession: B01427; A01427

R;Bodenmuller, H.; Schaller, H.C.

Nature 293, 579-580, 1981

A;Title: Conserved amino acid sequence of a neuropeptide, the head activator, from coelenterates to humans.

A;Reference number: A93266; MUID:82035850; PMID:7290191

A;Accession: B01427

A;Molecule type: protein  
 A;Residues: 1-11 <BOD>  
 R;Birrr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.  
 FEBS Lett. 131, 317-321, 1981  
 A;Title: Synthesis of a new neuropeptide, the head activator from hydra.  
 A;Reference number: A91296; MUID:82050803; PMID:7297679  
 A;Contents: annotation; synthesis  
 A;Note: the synthetic peptide was identical with the natural peptide in chemical structure and biological activity  
 C;Comment: This peptide was first isolated from nerve cells of hydra and was called head activator because it induced head-specific growth and differentiation in this animal. It has been found in mammalian intestine and hypothalamus.  
 C;Superfamily: unassigned animal peptides  
 C;Keywords: blocked amino end; growth factor; hormone; hypothalamus; intestine; neuropeptide  
 F;1/Modified site: blocked amino end (Gln) (probably pyrrolidone carboxylic acid) #status experimental

Query Match 18.2%; Score 2; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 3.4e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GG 4  
 ||  
 Db 4 GG 5

## RESULT 12

YHBO

morphogenetic neuropeptide - bovine

C;Species: Bos primigenius taurus (cattle)

C;Date: 20-Jun-2000 #sequence\_revision 20-Jun-2000 #text\_change 20-Jun-2000

C;Accession: C01427; A01427

R;Bodenmuller, H.; Schaller, H.C.

Nature 293, 579-580, 1981

A;Title: Conserved amino acid sequence of a neuropeptide, the head activator, from coelenterates to humans.

A;Reference number: A93266; MUID:82035850; PMID:7290191

A;Accession: C01427

A;Molecule type: protein

A;Residues: 1-11 <BOD>

R;Birrr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.

FEBS Lett. 131, 317-321, 1981

A;Title: Synthesis of a new neuropeptide, the head activator from hydra.

A;Reference number: A91296; MUID:82050803; PMID:7297679

A;Contents: annotation; synthesis

A;Note: the synthetic peptide was identical with the natural peptide in chemical structure and biological activity

C;Comment: This peptide was first isolated from nerve cells of hydra and was called head activator because it induced head-specific growth and differentiation in this animal. It has been found in mammalian intestine and hypothalamus.

C;Superfamily: unassigned animal peptides

C;Keywords: blocked amino end; growth factor; hormone; hypothalamus; intestine; neuropeptide

F;1/Modified site: blocked amino end (Gln) (probably pyrrolidone carboxylic acid) #status experimental

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.4e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GG 4  
||  
Db 4 GG 5

RESULT 13

YHXAE

morphogenetic neuropeptide - sea anemone (*Anthopleura elegantissima*)

N;Alternate names: head activator

C;Species: *Anthopleura elegantissima*

C;Date: 20-Jun-2000 #sequence\_revision 20-Jun-2000 #text\_change 20-Jun-2000

C;Accession: A93900; A01427

R;Schaller, H.C.; Bodenmuller, H.

Proc. Natl. Acad. Sci. U.S.A. 78, 7000-7004, 1981

A;Title: Isolation and amino acid sequence of a morphogenetic peptide from hydra.

A;Reference number: A93900

A;Accession: A93900

A;Molecule type: protein

A;Residues: 1-11 <SCH>

R;Birrr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.

FEBS Lett. 131, 317-321, 1981

A;Title: Synthesis of a new neuropeptide, the head activator from hydra.

A;Reference number: A91296; MUID:82050803; PMID:7297679

A;Contents: annotation; synthesis

A;Note: the synthetic peptide was identical with the natural peptide in chemical structure and biological activity

C;Comment: This peptide was first isolated from nerve cells of hydra and was called head activator because it induced head-specific growth and differentiation in this animal. It has also been found in mammalian intestine and hypothalamus.

C;Superfamily: unassigned animal peptides

C;Keywords: growth factor; hormone; neuropeptide; pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.4e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GG 4  
||  
Db 4 GG 5

RESULT 14

YHJFHY

morphogenetic neuropeptide - *Hydra attenuata*

N;Alternate names: head activator

C;Species: *Hydra attenuata*

C;Date: 20-Jun-2000 #sequence\_revision 20-Jun-2000 #text\_change 20-Jun-2000

C;Accession: B93900; A01427  
 R;Schaller, H.C.; Bodenmuller, H.  
 Proc. Natl. Acad. Sci. U.S.A. 78, 7000-7004, 1981  
 A;Title: Isolation and amino acid sequence of a morphogenetic peptide from hydra.  
 A;Reference number: A93900  
 A;Accession: B93900  
 A;Molecule type: protein  
 A;Residues: 1-11 <SCH>  
 R;Birrr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.  
 FEBS Lett. 131, 317-321, 1981  
 A;Title: Synthesis of a new neuropeptide, the head activator from hydra.  
 A;Reference number: A91296; MUID:82050803; PMID:7297679  
 A;Contents: annotation; synthesis  
 A;Note: the synthetic peptide was identical with the natural peptide in chemical structure and biological activity  
 C;Comment: This peptide was first isolated from nerve cells of hydra and was called head activator because it induced head-specific growth and differentiation in this animal. It has also been found in mammalian intestine and hypothalamus.  
 C;Superfamily: unassigned animal peptides  
 C;Keywords: growth factor; hormone; neuropeptide; pyroglutamic acid  
 F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 18.2%; Score 2; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 3.4e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GG 4  
 ||  
 Db 4 GG 5

#### RESULT 15

S42449  
 ant1 protein - phage P7  
 C;Species: phage P7  
 C;Date: 07-Sep-1994 #sequence\_revision 26-May-1995 #text\_change 08-Oct-1999  
 C;Accession: S42449  
 R;Citron, M.; Schuster, H.  
 Cell 62, 591-598, 1990  
 A;Title: The c4 repressors of bacteriophages P1 and P7 are antisense RNAs.  
 A;Reference number: S42448; MUID:90335968; PMID:1696181  
 A;Accession: S42449  
 A;Status: preliminary; translation not shown  
 A;Molecule type: DNA  
 A;Residues: 1-11 <CIT>  
 A;Cross-references: EMBL:M35139; NID:g215705; PIDN:AAA32437.1; PID:g215707

Query Match 18.2%; Score 2; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 3.4e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KK 6  
 ||  
 Db 2 KK 3

RESULT 16

C58501

42K bile stone protein - unidentified bacterium (fragment)

C;Species: unidentified bacterium

C;Date: 07-Feb-1997 #sequence\_revision 07-Feb-1997 #text\_change 10-Jul-1998

C;Accession: C58501

R;Binette, J.P.; Binette, M.B.

submitted to the Protein Sequence Database, October 1996

A;Description: The proteins of kidney and gallbladder stones.

A;Reference number: A58501

A;Accession: C58501

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-11 <BIN>

A;Experimental source: human bile with stones

A;Note: tentative identification of 1-Gly

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.4e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GG 4  
||  
Db 1 GG 2

RESULT 17

JQ0395

hypothetical protein (nodB 3' region) - Azorhizobium caulinodans

N;Alternate names: hypothetical 1.4K protein

C;Species: Azorhizobium caulinodans

A;Note: host Sesbania rostrata

C;Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 03-Feb-1994

C;Accession: JQ0395

R;Goethals, K.; Gao, M.; Tomekpe, K.; Van Montagu, M.; Holsters, M.

Mol. Gen. Genet. 219, 289-298, 1989

A;Title: Common nodABC genes in Nod locus 1 of Azorhizobium caulinodans: nucleotide sequence and plant-inducible expression.

A;Reference number: JQ0393; MUID:90136519; PMID:2615763

A;Accession: JQ0395

A;Molecule type: DNA

A;Residues: 1-11 <GOE>

A;Cross-references: GB:L18897

A;Experimental source: strain ORS571

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.4e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 MR 10  
||  
Db 1 MR 2

RESULT 18

PQ0231

beta-glucosidase (EC 3.2.1.21) - *Cellvibrio gilvus* (fragment)  
 C;Species: *Cellvibrio gilvus*  
 C;Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 07-May-1999  
 C;Accession: PQ0231  
 R;Kashiwagi, Y.; Iijima, C.; Sasaki, T.; Taniguchi, H.  
 Agric. Biol. Chem. 55, 2553-2559, 1991  
 A;Title: Characterization of a beta-glucosidase encoded by a gene from  
*Cellvibrio gilvus*.  
 A;Reference number: PQ0231; MUID:92144103; PMID:1368758  
 A;Accession: PQ0231  
 A;Molecule type: protein  
 A;Residues: 1-11 <KAS>  
 C;Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 18.2%; Score 2; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 3.4e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AE 2  
 ||  
 Db 5 AE 6

#### RESULT 19

S66606  
 quinoline 2-oxidoreductase alpha chain - *Comamonas testosteroni* (fragment)  
 C;Species: *Comamonas testosteroni*  
 C;Date: 15-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 17-Mar-1999  
 C;Accession: S66606  
 R;Schach, S.; Tshisuaka, B.; Fetzner, S.; Lingens, F.  
 Eur. J. Biochem. 232, 536-544, 1995  
 A;Title: Quinoline 2-oxidoreductase and 2-oxo-1,2-dihydroquinoline 5,6-  
 dioxygenase from *Comamonas testosteroni* 63. The first two enzymes in quinoline  
 and 3-methylquinoline degradation.  
 A;Reference number: S66606; MUID:96035889; PMID:7556204  
 A;Accession: S66606  
 A;Molecule type: protein  
 A;Residues: 1-11 <SCH>  
 A;Experimental source: strain 63

Query Match 18.2%; Score 2; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 3.4e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AE 2  
 ||  
 Db 6 AE 7

#### RESULT 20

S58244  
 pyrroloquinoline quinone synthesis C - *Pseudomonas fluorescens* (fragment)  
 C;Species: *Pseudomonas fluorescens*  
 C;Date: 13-Jan-1996 #sequence\_revision 01-Mar-1996 #text\_change 08-Oct-1999  
 C;Accession: S58244  
 R;Schnider, U.; Keel, C.; Defago, G.; Haas, D.  
 submitted to the EMBL Data Library, May 1995



A;Description: Tn5-directed cloning of pqq genes from *Pseudomonas fluorescens* CHA0: their involvement in the production of the antibiotic pyoluteorin.

A;Reference number: S58239

A;Accession: S58244

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-11 <SCH>

A;Cross-references: EMBL:X87299; NID:g929799; PIDN:CAA60734.1; PID:g929806

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.4e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AE 2  
||  
Db 9 AE 10

#### RESULT 21

S04875

nifS protein - *Bradyrhizobium japonicum* (fragment)

C;Species: *Bradyrhizobium japonicum*

C;Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 08-Oct-1999

C;Accession: S04875

R;Ebeling, S.

submitted to the EMBL Data Library, December 1988

A;Reference number: S04873

A;Accession: S04875

A;Molecule type: DNA

A;Residues: 1-11 <EBE>

A;Cross-references: EMBL:X13691; NID:g39544; PIDN:CAA31982.1; PID:g580775

C;Genetics:

A;Gene: nifS

A;Start codon: GTG

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.4e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 RA 11  
||  
Db 5 RA 6

#### RESULT 22

E60691

phycobilisome 8K linker protein - *Synechococcus* sp. (PCC 7002) (fragment)

C;Species: *Synechococcus* sp.

C;Date: 14-May-1993 #sequence\_revision 14-May-1993 #text\_change 07-May-1999

C;Accession: E60691

R;Bryant, D.A.; de Lorimier, R.; Guglielmi, G.; Stevens Jr., S.E.

Arch. Microbiol. 153, 550-560, 1990

A;Title: Structural and compositional analyses of the phycobilisomes of *Synechococcus* sp. PCC 7002. Analyses of the wild-type strain and a phycocyanin-less mutant constructed by interposon mutagenesis.

A;Reference number: A60691; MUID:90314662; PMID:2164365

A;Accession: E60691

A;Molecule type: protein  
A;Residues: 1-11 <BRY>  
C;Comment: This protein, one of the eleven components detected in this species of the phycobilisome that helps to trap light energy for photosystem II, does not carry a chromophore.  
C;Keywords: photosystem II

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.4e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 MR 10  
||  
Db 1 MR 2

#### RESULT 23

S33519

probable secreted protein - *Acholeplasma laidlawii* (fragment)

C;Species: *Acholeplasma laidlawii*

C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 22-Oct-1999

C;Accession: S33519

R;Boyer, M.J.; Jarhede, T.K.; Tegman, V.; Wieslander, A.

submitted to the EMBL Data Library, June 1993

A;Description: Sequence regions from *Acholeplasma laidlawii* which restore export of beta-lactamase in *Escherichia coli*.

A;Reference number: S33518

A;Accession: S33519

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-11 <BOY>

A;Cross-references: EMBL:Z22875; NID:g311706; PIDN:CAA80495.1; PID:g311708

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.4e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KK 6  
||  
Db 2 KK 3

#### RESULT 24

T06383

hypothetical protein - soybean

C;Species: *Glycine max* (soybean)

C;Date: 30-Apr-1999 #sequence\_revision 30-Apr-1999 #text\_change 11-May-2000

C;Accession: T06383

R;Dewey, R.E.; Wilson, R.F.; Novitzky, W.P.; Goode, J.H.

Plant Cell 6, 1495-1507, 1994

A;Title: The AAPT1 gene of soybean complements a cholinephosphotransferase-deficient mutant of yeast.

A;Reference number: Z06169; MUID:95086383; PMID:7994181

A;Accession: T06383

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-11 <DEW>

A;Cross-references: EMBL:U12735; NID:g530086; PIDN:AAA67718.1; PID:g530087  
A;Experimental source: strain Dare; seed

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.4e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KM 9  
||  
Db 2 KM 3

RESULT 25

S19775

wound-induced protein - tomato (fragment)

C;Species: Lycopersicon esculentum (tomato)

C;Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 09-Sep-1997

C;Accession: S19775

R;Parsons, B.L.

submitted to the EMBL Data Library, May 1991

A;Reference number: S19773

A;Accession: S19775

A;Molecule type: mRNA

A;Residues: 1-11 <PAR>

A;Cross-references: EMBL:X59884; NID:g19323; PID:g19324

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.4e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KK 6  
||  
Db 5 KK 6

RESULT 26

S41747

chaperonin 10 homolog - potato (fragment)

C;Species: Solanum tuberosum (potato)

C;Date: 19-Mar-1997 #sequence\_revision 29-Aug-1997 #text\_change 07-May-1999

C;Accession: S41747

R;Burt, W.J.E.; Leaver, C.J.

FEBS Lett. 339, 139-141, 1994

A;Title: Identification of a chaperonin-10 homologue in plant mitochondria.

A;Reference number: S41747; MUID:94148071; PMID:7906228

A;Accession: S41747

A;Molecule type: protein

A;Residues: 1-11 <BUR>

A;Experimental source: mitochondrion

C;Keywords: mitochondrion; molecular chaperone

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.4e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GG 4  
||

Db 7 GG 8

RESULT 27

A38590

transforming protein (Ddras) - slime mold (*Dictyostelium discoideum*) (fragment)

C;Species: *Dictyostelium discoideum*

C;Date: 18-Oct-1991 #sequence\_revision 18-Oct-1991 #text\_change 30-Sep-1993

C;Accession: A38590

R;Esch, R.K.; Firtel, R.A.

Genes Dev. 5, 9-21, 1991

A;Title: cAMP and cell sorting control the spatial expression of a developmentally essential cell-type-specific ras gene in *Dictyostelium*.

A;Reference number: A38590; MUID:91115102; PMID:1703508

A;Accession: A38590

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-11 <ESC>

A;Cross-references: GB:Z11804; GB:K02114; GB:X58190

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.4e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GG 4  
||  
Db 10 GG 11

RESULT 28

A61512

variant surface glycoprotein MITat 1.7 - *Trypanosoma brucei* (fragment)

C;Species: *Trypanosoma brucei*

C;Date: 28-Oct-1994 #sequence\_revision 28-Oct-1994 #text\_change 07-May-1999

C;Accession: A61512

R;Holder, A.A.; Cross, G.A.M.

Mol. Biochem. Parasitol. 2, 135-150, 1981

A;Title: Glycopeptides from variant surface glycoproteins of *Trypanosoma brucei*. C-terminal location of antigenically cross-reacting carbohydrate moieties.

A;Reference number: A61512; MUID:81172836; PMID:6163983

A;Accession: A61512

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-11 <HOL>

C;Keywords: glycoprotein

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.4e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AE 2  
||  
Db 3 AE 4

RESULT 29

A35594

buccalin - California sea hare  
 C;Species: Aplysia californica (California sea hare)  
 C;Date: 14-Sep-1990 #sequence\_revision 14-Sep-1990 #text\_change 24-Jun-1993  
 C;Accession: A35594  
 R;Cropper, E.C.; Miller, M.W.; Tenenbaum, R.; Kolks, M.A.G.; Kupfermann, I.; Weiss, K.R.  
 Proc. Natl. Acad. Sci. U.S.A. 85, 6177-6181, 1988  
 A;Title: Structure and action of buccalin: a modulatory neuropeptide localized to an identified small cardioactive peptide-containing cholinergic motor neuron of Aplysia californica.  
 A;Reference number: A35594; MUID:88320404; PMID:3413086  
 A;Accession: A35594  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-11 <CRO>

Query Match 18.2%; Score 2; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 3.4e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GG 4  
 ||  
 Db 9 GG 10

#### RESULT 30

A60656

perisulfakinin - American cockroach

C;Species: Periplaneta americana (American cockroach)

C;Date: 14-May-1993 #sequence\_revision 14-May-1993 #text\_change 11-Jul-1997

C;Accession: A60656

R;Veenstra, J.A.

Neuropeptides 14, 145-149, 1989

A;Title: Isolation and structure of two gastrin/CCK-like neuropeptides from the American cockroach homologous to the leucosulfakinins.

A;Reference number: A60656; MUID:90137190; PMID:2615921

A;Accession: A60656

A;Molecule type: protein

A;Residues: 1-11 <VEE>

C;Comment: This neuropeptide stimulates hindgut contractions.

C;Keywords: amidated carboxyl end; neuropeptide; sulfoprotein

F;6/Binding site: sulfate (Tyr) (covalent) #status experimental

F;11/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 18.2%; Score 2; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 3.4e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 MR 10  
 ||  
 Db 9 MR 10

#### RESULT 31

S65395

chemical-sense-related lipophilic-ligand-binding protein - fruit fly (Drosophila melanogaster) (fragment)

C;Species: *Drosophila melanogaster*  
 C;Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 07-May-1999  
 C;Accession: S65395  
 R;Ozaki, M.; Morisaki, K.; Idei, W.; Ozaki, K.; Tokunaga, F.  
 Eur. J. Biochem. 230, 298-308, 1995  
 A;Title: A putative lipophilic stimulant carrier protein commonly found in the taste and olfactory systems. A unique member of the pheromone-binding protein superfamily.  
 A;Reference number: S65394; MUID:95324537; PMID:7601113  
 A;Accession: S65395  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-11 <OZA>

Query Match 18.2%; Score 2; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 3.4e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AE 2  
 ||  
 Db 10 AE 11

#### RESULT 32

I41978  
 calliFMRFamide 9 - bluebottle fly (*Calliphora vomitoria*)  
 C;Species: *Calliphora vomitoria*  
 C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 17-Mar-1999  
 C;Accession: I41978  
 R;Duve, H.; Johnsen, A.H.; Sewell, J.C.; Scott, A.G.; Orchard, I.; Rehfeld, J.F.; Thorpe, A.  
 Proc. Natl. Acad. Sci. U.S.A. 89, 2326-2330, 1992  
 A;Title: Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH-2 neuropeptides (designated calliFMRFamides) from the blowfly *Calliphora vomitoria*.  
 A;Reference number: A41978; MUID:92196111; PMID:1549595  
 A;Accession: I41978  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-11 <DUV>  
 C;Keywords: amidated carboxyl end; neuropeptide  
 F;11/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 18.2%; Score 2; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 3.4e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 MR 10  
 ||  
 Db 9 MR 10

#### RESULT 33

D37196  
 bradykinin-potentiating peptide 4 - island jararaca  
 C;Species: *Bothrops insularis* (island jararaca)  
 C;Date: 14-Feb-1992 #sequence\_revision 01-Dec-1992 #text\_change 05-Aug-1994

C;Accession: D37196  
R;Cintra, A.C.O.; Vieira, C.A.; Giglio, J.R.  
J. Protein Chem. 9, 221-227, 1990  
A;Title: Primary structure and biological activity of bradykinin potentiating peptides from Bothrops insularis snake venom.  
A;Reference number: A37196; MUID:90351557; PMID:2386615  
A;Accession: D37196  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-11 <CIN>  
C;Keywords: pyroglutamic acid  
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.4e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GG 4  
||  
Db 2 GG 3

RESULT 34

I65231  
CCK-B gastrin receptor isoform - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 21-Jul-2000  
C;Accession: I65231  
R;Miyake, A.  
Biochem. Biophys. Res. Commun. 208, 230-237, 1995  
A;Title: A truncated isoform of human CCK-B/gastrin receptor generated by alternative usage of a novel exon.  
A;Reference number: I52307; MUID:95194412; PMID:7887934  
A;Accession: I65231  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: mRNA  
A;Residues: 1-11 <RES>  
A;Cross-references: GB:S76072; NID:g913752; PIDN:AAB33740.1; PID:g913753  
C;Genetics:  
A;Gene: CCK-B

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.4e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GG 4  
||  
Db 4 GG 5

RESULT 35

PT0249  
Ig heavy chain CRD3 region (clone 2-109A) - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996  
C;Accession: PT0249  
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.

J. Exp. Med. 173, 395-407, 1991

A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and joining segments in adult human peripheral blood B lymphocytes.

A;Reference number: PT0222; MUID:91108337; PMID:1899102

A;Accession: PT0249

A;Molecule type: DNA

A;Residues: 1-11 <YAM>

A;Experimental source: B lymphocyte

C;Keywords: heterotetramer; immunoglobulin

Query Match 18.2%; Score 2; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 3.4e+04;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GG 4

||

Db 1 GG 2

#### RESULT 36

PT0302

Ig heavy chain CRD3 region (clone 5-112) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996

C;Accession: PT0302

R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.

J. Exp. Med. 173, 395-407, 1991

A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and joining segments in adult human peripheral blood B lymphocytes.

A;Reference number: PT0222; MUID:91108337; PMID:1899102

A;Accession: PT0302

A;Molecule type: DNA

A;Residues: 1-11 <YAM>

A;Experimental source: B lymphocyte

C;Keywords: heterotetramer; immunoglobulin

Query Match 18.2%; Score 2; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 3.4e+04;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GG 4

||

Db 2 GG 3

#### RESULT 37

PH1343

Ig heavy chain DJ region (clone C100-91) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999

C;Accession: PH1343

R;Wasserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.

J. Exp. Med. 176, 1577-1581, 1992

A;Title: Predominance of fetal type DJH joining in young children with B precursor lymphoblastic leukemia as evidence for an in utero transforming event.

A;Reference number: PH1302; MUID:93094761; PMID:1460419

A;Accession: PH1343



A;Molecule type: DNA  
A;Residues: 1-11 <WAS>  
C;Keywords: heterotetramer; immunoglobulin

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.4e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GG 4  
||  
Db 1 GG 2

RESULT 38

S51732

T-cell receptor alpha chain joining region - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 07-May-1995 #sequence\_revision 01-Sep-1995 #text\_change 05-Nov-1999

C;Accession: S51732

R;Durinovic-Bello, I.; Steinle, A.; Ziegler, A.G.; Schendel, D.J.  
submitted to the EMBL Data Library, November 1993

A;Reference number: S51732

A;Accession: S51732

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-11 <DUR>

A;Cross-references: EMBL:Z28343; NID:g607116; PIDN:CAA82197.1; PID:g607117

C;Keywords: T-cell receptor

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.4e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GK 5  
||  
Db 7 GK 8

RESULT 39

S60354

retinal oxidase - rabbit (fragment)

C;Species: Oryctolagus cuniculus (domestic rabbit)

C;Date: 24-Aug-1996 #sequence\_revision 13-Mar-1997 #text\_change 13-Mar-1997

C;Accession: S60354

R;Huang, D.Y.; Ichikawa, Y.

Biochim. Biophys. Acta 1243, 431-436, 1995

A;Title: Identification of essential lysyl and cysteinyl residues, and the amino acid sequence at the substrate-binding site of retinal oxidase.

A;Reference number: S60354; MUID:95244596; PMID:7727518

A;Accession: S60354

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-11 <HUA>

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.4e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy            3 GG 4  
              ||  
Db            1 GG 2

RESULT 40

PN0044

protein kinase C inhibitor I - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 29-Oct-1997 #sequence\_revision 29-Oct-1997 #text\_change 23-Jan-1998

C;Accession: PN0044

R;Kato, H.

Kawasaki Igakkaishi 22, 245-259, 1996

A;Title: Analysis of proteins isolated by two dimensional electrophoresis of mouse neuroblastoma cells.

A;Reference number: PN0041

A;Accession: PN0044

A;Molecule type: protein

A;Residues: 1-11 <KAT>

A;Experimental source: neuroblastoma cell

C;Comment: The molecular mass is 13,900 and the pI is 6.36. The amino-terminus is blocked.

C;Keywords: brain

Query Match                    18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity       100.0%; Pred. No. 3.4e+04;  
Matches       2; Conservative    0; Mismatches    0; Indels       0; Gaps       0;

Qy            3 GG 4  
              ||  
Db            8 GG 9

RESULT 41

PT0209

T-cell receptor alpha chain V-J region (4-1-L.6) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 30-May-1997

C;Accession: PT0209

R;Nakano, N.; Kikutani, H.; Nishimoto, H.; Kishimoto, T.

J. Exp. Med. 173, 1091-1097, 1991

A;Title: T cell receptor V gene usage of islet beta cell-reactive T cells is not restricted in non-obese diabetic mice.

A;Reference number: PT0209; MUID:91217621; PMID:1902501

A;Accession: PT0209

A;Molecule type: mRNA

A;Residues: 1-11 <NAK>

C;Keywords: T-cell receptor

Query Match                    18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity       100.0%; Pred. No. 3.4e+04;  
Matches       2; Conservative    0; Mismatches    0; Indels       0; Gaps       0;

Qy            2 EG 3  
              ||  
Db            4 EG 5

# RESULT 42

PT0218

T-cell receptor beta chain V-J region (7-10-D.3) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 30-May-1997

C;Accession: PT0218

R;Nakano, N.; Kikutani, H.; Nishimoto, H.; Kishimoto, T.

J. Exp. Med. 173, 1091-1097, 1991

A;Title: T cell receptor V gene usage of islet beta cell-reactive T cells is not restricted in non-obese diabetic mice.

A;Reference number: PT0209; MUID:91217621; PMID:1902501

A;Accession: PT0218

A;Molecule type: mRNA

A;Residues: 1-11 <NAK>

C;Keywords: T-cell receptor

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.4e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GG 4

||

Db 6 GG 7

# RESULT 43

I41946

T-cell receptor gamma chain (5t.1) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 07-May-1999

C;Accession: I41946

R;Whetsell, M.; Mosley, R.L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.

Mol. Cell. Biol. 11, 5902-5909, 1991

A;Title: Rearrangement and junctional-site sequence analyses of T-cell receptor gamma genes in intestinal intraepithelial lymphocytes from murine athymic chimeras.

A;Reference number: A41946; MUID:92049316; PMID:1658619

A;Accession: I41946

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: DNA

A;Residues: 1-11 <WHE>

C;Keywords: T-cell receptor

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.4e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GG 4

||

Db 5 GG 6

# RESULT 44

C49037

TcR gamma V-J region - mouse (fragment)  
 C;Species: Mus musculus (house mouse)  
 C;Date: 21-Jan-1994 #sequence\_revision 18-Nov-1994 #text\_change 05-Nov-1999  
 C;Accession: C49037  
 R;Ezquerria, A.; Wilde, D.B.; McConnell, T.J.; Sturmhofel, K.; Valas, R.B.;  
 Shevach, E.M.; Coligan, J.E.  
 Eur. J. Immunol. 22, 491-498, 1992  
 A;Title: Mouse autoreactive gamma/delta T cells. II. Molecular characterization  
 of the T cell receptor.  
 A;Reference number: A49037; MUID:92164730; PMID:1311262  
 A;Accession: C49037  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-11 <EZQ>  
 A;Cross-references: GB:S90639; NID:g246292; PIDN:AAB21549.1; PID:g246293  
 A;Experimental source: dendritic epidermal T-cell lines  
 A;Note: sequence extracted from NCBI backbone (NCBIN:90639, NCBIP:90645)

Query Match 18.2%; Score 2; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 3.4e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GG 4  
 ||  
 Db 6 GG 7

#### RESULT 45

PD0441

translation elongation factor TU-like protein P43, mitochondrial - mouse  
 (fragment)

C;Species: Mus musculus (house mouse)  
 C;Date: 21-Aug-1998 #sequence\_revision 21-Aug-1998 #text\_change 21-Aug-1998  
 C;Accession: PD0441  
 R;Kawakami, T.; Uchida, T.; Sakai, T.; Kamo, M.; Morimasa, T.; Tsugita, A.  
 submitted to JIPID, August 1998  
 A;Description: Proteome analysis of mouse brain.  
 A;Reference number: PD0441  
 A;Accession: PD0441  
 A;Molecule type: protein  
 A;Residues: 1-11 <KAW>  
 A;Experimental source: striatum  
 C;Keywords: mitochondrion

Query Match 18.2%; Score 2; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 3.4e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KK 6  
 ||  
 Db 5 KK 6

#### RESULT 46

I77447

urinary protein - mouse (fragment)  
 C;Species: Mus musculus (house mouse)

C;Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 05-Nov-1999  
 C;Accession: I77447; I77448  
 R;Held, W.A.; Gallagher, J.F.; Hohman, C.M.; Kuhn, N.J.; Sampsell, B.M.; Hughes, R.G.  
 Mol. Cell. Biol. 7, 3705-3712, 1987  
 A;Title: Identification and characterization of functional genes encoding the mouse major urinary proteins.  
 A;Reference number: I57627; MUID:88065510; PMID:2824995  
 A;Accession: I77447  
 A;Status: preliminary; translated from GB/EMBL/DDBJ  
 A;Molecule type: DNA  
 A;Residues: 1-11 <RES>  
 A;Cross-references: GB:M17815; NID:g202301; PIDN:AAA40541.1; PID:g202302  
 A;Accession: I77448  
 A;Status: preliminary; translated from GB/EMBL/DDBJ  
 A;Molecule type: DNA  
 A;Residues: 1-11 <RE2>  
 A;Cross-references: GB:M17816; NID:g202303; PIDN:AAA40542.1; PID:g202304

Query Match 18.2%; Score 2; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 3.4e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KM 9  
 ||  
 Db 2 KM 3

#### RESULT 47

S65377

cytochrome-c oxidase (EC 1.9.3.1) chain VIa-H, cardiac - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 16-Jul-1999

C;Accession: S65377

R;Schaeffer, H.; Noack, H.; Halangk, W.; Brandt, U.; von Jagow, G.

Eur. J. Biochem. 230, 235-241, 1995

A;Title: Cytochrome-c oxidase in developing rat heart. Enzymic properties and amino-terminal sequences suggest identity of the fetal heart and the adult liver isoform.

A;Reference number: S65372; MUID:95324529; PMID:7601105

A;Accession: S65377

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-11 <SCH>

C;Keywords: cardiac muscle; heart; oxidoreductase

Query Match 18.2%; Score 2; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 3.4e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GG 4  
 ||  
 Db 8 GG 9

#### RESULT 48

S78422

ribosomal protein RS20, mitochondrial [validated] - rat (tentative sequence)  
(fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 25-Feb-1998 #sequence\_revision 13-Mar-1998 #text\_change 21-Jul-2000

C;Accession: S78422

R;Goldschmidt-Reisin, S.; Graack, H.R.

submitted to the Protein Sequence Database, February 1998

A;Reference number: S78411

A;Accession: S78422

A;Molecule type: protein

A;Residues: 1-11 <GOL>

A;Note: the protein is designated as mitochondrial ribosomal protein S20

C;Keywords: mitochondrion; protein biosynthesis; ribosome

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.4e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 MR 10  
||  
Db 1 MR 2

#### RESULT 49

PH0947

T-cell receptor beta chain V-D-J region (clone A2) - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 09-Oct-1992 #sequence\_revision 09-Oct-1992 #text\_change 30-May-1997

C;Accession: PH0947

R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.  
J. Exp. Med. 174, 1467-1476, 1991

A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental  
allergic encephalomyelitis: conserved complementarity determining region 3.

A;Reference number: PH0891; MUID:92078857; PMID:1836012

A;Accession: PH0947

A;Molecule type: mRNA

A;Residues: 1-11 <GOL>

A;Experimental source: myelin basic protein fragment-reactive T-cell, recovered  
from experimentally induced allergic encephalomyelitis

C;Keywords: T-cell receptor

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.4e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GG 4  
||  
Db 6 GG 7

#### RESULT 50

I52304

gene rSSTR4 protein - rat (fragment)

C;Species: Rattus sp. (rat)

C;Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 17-Mar-1999

C;Accession: I52304

R;Xu, Y.; Bruno, J.F.; Berelowitz, M.

Biochem. Biophys. Res. Commun. 206, 935-941, 1995  
A;Title: Characterization of the proximal promoter region of the rat  
somatostatin receptor gene, SSTR4.  
A;Reference number: I52304; MUID:95134278; PMID:7832807  
A;Accession: I52304  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-11 <RES>  
A;Cross-references: GB:S75475; NID:g914315  
C;Genetics:  
A;Gene: rSSTR4

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.4e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GG 4  
||  
Db 10 GG 11

RESULT 51

A34243

H-hyosophorin - Japanese flounder (fragment)  
C;Species: Paralichthys olivaceus (Japanese flounder)  
C;Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 12-Feb-1999  
C;Accession: A34243  
R;Seko, A.; Kitajima, K.; Iwasaki, M.; Inoue, S.; Inoue, Y.  
J. Biol. Chem. 264, 15922-15929, 1989  
A;Title: Structural studies of fertilization-associated carbohydrate-rich  
glycoproteins (Hyosophorin) isolated from the fertilized and unfertilized eggs  
of flounder, Paralichthys olivaceus. Presence of a novel penta-antennary N-  
linkedglycan chain in the tandem repeating glycopeptide unit of hyosophorin.  
A;Reference number: A34243; MUID:89380184; PMID:2777771  
A;Accession: A34243  
A;Molecule type: protein  
A;Residues: 1-11 <SEK>  
A;Note: 3-Ala, 4-Ala, 5-Pro or Gln, and 6-Val were also found

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.4e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GG 4  
||  
Db 5 GG 6

RESULT 52

A61575

Trimeresurus serine proteinase (EC 3.4.21.-) - Sakishima habu (fragment)  
N;Alternate names: hemorrhagic toxin  
C;Species: Trimeresurus elegans (Sakishima habu)  
C;Date: 20-Oct-1994 #sequence\_revision 06-Jan-1995 #text\_change 06-Jan-1995  
C;Accession: A61575  
R;Nikai, T.; Komori, Y.; Imai, K.; Sugihara, H.  
Int. J. Biochem. 23, 73-78, 1991

A;Title: Isolation and characterization of hemorrhagic toxin from the venom of *Trimeresurus elegans*.

A;Reference number: A61575; MUID:91216327; PMID:2022298

A;Accession: A61575

A;Molecule type: protein

A;Residues: 1-11 <NIK>

C;Keywords: hydrolase; serine proteinase; venom

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.4e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GG 4  
||  
Db 3 GG 4

#### RESULT 53

S19015

hypothetical protein 11 ruvC-yebC intergenic region - *Escherichia coli*

C;Species: *Escherichia coli*

C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999

C;Accession: S19015

R;Sharples, G.J.; Lloyd, R.G.

J. Bacteriol. 173, 7711-7715, 1991

A;Title: Resolution of Holliday junctions in *Escherichia coli*: identification of the ruvC gene product as a 19-kilodalton protein.

A;Reference number: S19013; MUID:92041688; PMID:1657895

A;Accession: S19015

A;Molecule type: DNA

A;Residues: 1-11 <SHA>

A;Cross-references: EMBL:X59551; NID:g42172; PIDN:CAA42127.1; PID:g42174

C;Comment: This is the hypothetical translation of a sequence that was not reported as a coding sequence in the complete genome.

Query Match 18.2%; Score 2; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.4e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 MR 10  
||  
Db 1 MR 2

#### RESULT 54

I54081

retinoic acid receptor alpha, exon 3 (mistranslated) - human (fragment)

C;Species: *Homo sapiens* (man)

C;Date: 04-Jun-1999 #sequence\_revision 04-Jun-1999 #text\_change 28-Jun-1999

C;Accession: I54081

R;Dong, S.; Geng, J.P.; Tong, J.H.; Wu, Y.; Cai, J.R.; Sun, G.L.; Chen, S.R.;

Wang, Z.Y.; Larsen, C.J.; Berger, R.

Genes Chromosomes Cancer 6, 133-139, 1993

A;Title: Breakpoint clusters of the PML gene in acute promyelocytic leukemia: primary structure of the reciprocal products of the PML-RARA gene in a patient with t(15;17).

A;Reference number: I54081; MUID:93222087; PMID:7682097



A;Accession: I54081  
A;Status: translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-11 <DON>  
A;Cross-references: GB:S57794; NID:g299073; PIDN:AAD13888.1; PID:g4261588  
A;Note: the translation is from an incorrect reading frame  
C;Genetics:  
A;Gene: GDB:RARA  
A;Cross-references: GDB:120337; OMIM:180240  
A;Map position: 17q12-17q12

Query Match 18.2%; Score 2; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.4e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 RA 11  
||  
Db 5 RA 6

RESULT 55

XAVIBH

bradykinin-potentiating peptide - halys viper

N;Alternate names: BPP

C;Species: Agkistrodon halys (halys viper)

C;Date: 30-Sep-1988 #sequence\_revision 30-Sep-1988 #text\_change 05-Aug-1994

C;Accession: JC0002

R;Chi, C.W.; Wang, S.Z.; Xu, L.G.; Wang, M.Y.; Lo, S.S.; Huang, W.D.

Peptides 6, 339-342, 1985

A;Title: Structure-function studies on the bradykinin potentiating peptide from Chinese snake venom (Agkistrodon halys Pallas).

A;Reference number: JC0002; MUID:86177022; PMID:3008123

A;Accession: JC0002

A;Molecule type: protein

A;Residues: 1-11 <CHI>

C;Comment: Because this peptide both inhibits the activity of the angiotensin-converting enzyme and enhances the action of bradykinin, it is an antihypertensive agent.

C;Superfamily: bradykinin-potentiating peptide

C;Keywords: angiotensin-converting enzyme inhibitor; antihypertensive; bradykinin; pyroglutamic acid; venom

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 G 3  
|  
Db 2 G 2

RESULT 56

XASNBA

bradykinin-potentiating peptide B - mamushi

C;Species: Agkistrodon blomhoffi (mamushi)

C;Date: 13-Jul-1981 #sequence\_revision 13-Jul-1981 #text\_change 08-Dec-1995

C;Accession: A01254  
R;Kato, H.; Suzuki, T.  
Proc. Jpn. Acad. 46, 176-181, 1970  
A;Reference number: A01254  
A;Accession: A01254  
A;Molecule type: protein  
A;Residues: 1-11 <KAT>  
A;Note: the sequence of the natural peptide was confirmed by the synthesis and analysis of a peptide having the identical structure and biological properties  
C;Superfamily: bradykinin-potentiating peptide  
C;Keywords: angiotensin-converting enzyme inhibitor; bradykinin; pyroglutamic acid; venom  
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 G 3  
|  
Db 2 G 2

#### RESULT 57

ECLQ2M

tachykinin II - migratory locust

C;Species: Locusta migratoria (migratory locust)

C;Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 08-Dec-1995

C;Accession: S08266

R;Schoofs, L.; Holman, G.M.; Hayes, T.K.; Nachman, R.J.; de Loof, A.

FEBS Lett. 261, 397-401, 1990

A;Title: Locustatachykinin I and II, two novel insect neuropeptides with homology to peptides of the vertebrate tachykinin family.

A;Reference number: S08265; MUID:90184489; PMID:2311766

A;Accession: S08266

A;Molecule type: protein

A;Residues: 1-11 <SCH>

C;Superfamily: tachykinin

C;Keywords: amidated carboxyl end; neuropeptide; tachykinin

F;11/Modified site: amidated carboxyl end (Arg) #status experimental

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1  
|  
Db 1 A 1

#### RESULT 58

SPHO

substance P - horse

C;Species: Equus caballus (domestic horse)

C;Date: 23-Oct-1981 #sequence\_revision 23-Oct-1981 #text\_change 23-Aug-1996

C;Accession: A01558

R;Studer, R.O.; Trzeciak, A.; Lergier, W.

Helv. Chim. Acta 56, 860-866, 1973

A;Title: Isolierung und Aminosaeuresequenz von Substanz P aus Pferdedarm.

A;Reference number: A01558

A;Accession: A01558

A;Molecule type: protein

A;Residues: 1-11 <STU>

C;Superfamily: substance P precursor

C;Keywords: amidated carboxyl end; hormone

F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 9.1%; Score 1; DB 1; Length 11;

Best Local Similarity 100.0%; Pred. No. 2e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 R 10

|

Db 1 R 1

#### RESULT 59

EOOCC

eledoisin - curled octopus

C;Species: Eledone cirrosa, Ozaena cirrosa (curled octopus)

C;Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 20-Mar-1998

C;Accession: B01561; A01561

R;Anastasi, A.; Erspamer, V.

Arch. Biochem. Biophys. 101, 56-65, 1963

A;Title: The isolation and amino acid sequence of eledoisin, the active endecapeptide of the posterior salivary glands of Eledone.

A;Reference number: A01561

A;Accession: B01561

A;Molecule type: protein

A;Residues: 1-11 <ANA>

C;Superfamily: substance P precursor

C;Keywords: amidated carboxyl end; hormone; pyroglutamic acid; salivary gland; secretagogue; vasodilator; venom

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 9.1%; Score 1; DB 1; Length 11;

Best Local Similarity 100.0%; Pred. No. 2e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 K 5

|

Db 4 K 4

#### RESULT 60

A60654

substance P - guinea pig

C;Species: Cavia porcellus (guinea pig)

C;Date: 14-May-1993 #sequence\_revision 27-Jun-1994 #text\_change 08-Dec-1995

C;Accession: A60654

R;Murphy, R.

Neuropeptides 14, 105-110, 1989

A;Title: Primary amino acid sequence of guinea-pig substance P.

A;Reference number: A60654; MUID:90044685; PMID:2478925  
A;Accession: A60654  
A;Molecule type: protein  
A;Residues: 1-11 <MUR>  
C;Superfamily: substance P precursor  
C;Keywords: amidated carboxyl end; neuropeptide; tachykinin  
F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 R 10  
|  
Db 1 R 1

#### RESULT 61

EOOC

eledoisin - musky octopus

C;Species: Eledone moschata, Ozaena moschata (musky octopus)

C;Date: 13-Jul-1981 #sequence\_revision 13-Jul-1981 #text\_change 20-Mar-1998

C;Accession: A01561

R;Anastasi, A.; Erspamer, V.

Arch. Biochem. Biophys. 101, 56-65, 1963

A;Title: The isolation and amino acid sequence of eledoisin, the active endecapeptide of the posterior salivary glands of Eledone.

A;Reference number: A01561

A;Accession: A01561

A;Molecule type: protein

A;Residues: 1-11 <ANA>

C;Superfamily: substance P precursor

C;Keywords: amidated carboxyl end; hormone; pyroglutamic acid; salivary gland; secretagogue; vasodilator; venom

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 K 5  
|  
Db 4 K 4

#### RESULT 62

LFTWWE

probable trpEG leader peptide - Thermus aquaticus

C;Species: Thermus aquaticus

C;Date: 30-Jun-1991 #sequence\_revision 30-Jun-1991 #text\_change 16-Jul-1999

C;Accession: S03315

R;Sato, S.; Nakada, Y.; Kanaya, S.; Tanaka, T.

Biochim. Biophys. Acta 950, 303-312, 1988

A;Title: Molecular cloning and nucleotide sequence of Thermus thermophilus HB8 trpE and trpG.

A;Reference number: S03315; MUID:89000781; PMID:2844259

A;Accession: S03315  
A;Molecule type: DNA  
A;Residues: 1-11 <SAT>  
A;Cross-references: EMBL:X07744; NID:g48261; PIDN:CAA30565.1; PID:g48262  
A;Note: the source is designated as *Thermus thermophilus* HB8  
C;Genetics:  
A;Gene: trpL  
C;Superfamily: probable trpEG leader peptide

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 M 9  
|  
Db 1 M 1

RESULT 63

G42762

proteasome endopeptidase complex (EC 3.4.25.1) subunit 13 - bovine (fragment)

C;Species: *Bos primigenius taurus* (cattle)

C;Date: 04-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 17-Feb-2003

C;Accession: G42762

R;Dick, L.R.; Moomaw, C.R.; Pramanik, B.C.; DeMartino, G.N.; Slaughter, C.A.  
Biochemistry 31, 7347-7355, 1992

A;Title: Identification and localization of a cysteinyl residue critical for the  
trypsin-like catalytic activity of the proteasome.

A;Reference number: A42762; MUID:92378961; PMID:1510924

A;Accession: G42762

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-11 <DIC>

A;Note: sequence extracted from NCBI backbone (NCBIP:112176)

C;Superfamily: multicatalytic endopeptidase complex chain C9

C;Keywords: hydrolase

Query Match 9.1%; Score 1; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 K 5  
|  
Db 8 K 8

RESULT 64

S68392

H+-transporting two-sector ATPase (EC 3.6.3.14) chain I - *Chlamydomonas*  
*reinhardtii* chloroplast (fragment)

N;Alternate names: ATP synthase chain I

C;Species: chloroplast *Chlamydomonas reinhardtii*

C;Date: 04-Dec-1997 #sequence\_revision 12-Dec-1997 #text\_change 03-Jun-2002

C;Accession: S68392

R;Fiedler, H.R.; Schmid, R.; Leu, S.; Shavit, N.; Strotmann, H.

FEBS Lett. 377, 163-166, 1995

A;Title: Isolation of CF(0)CF(1) from Chlamydomonas reinhardtii cw15 and the N-terminal amino acid sequences of the CF(0)CF(1) subunits.  
A;Reference number: S68388; MUID:96128220; PMID:8543042  
A;Accession: S68392  
A;Molecule type: protein  
A;Residues: 1-11 <FIE>  
A;Experimental source: strain CW15  
C;Genetics:  
A;Genome: chloroplast  
C;Superfamily: H<sup>+</sup>-transporting ATP synthase protein 6  
C;Keywords: ATP biosynthesis; chloroplast; hydrolase; membrane-associated complex; thylakoid

Query Match 9.1%; Score 1; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 E 2  
|  
Db 1 E 1

RESULT 65

B49164

chromogranin-B - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 19-Dec-1993 #sequence\_revision 18-Nov-1994 #text\_change 31-Oct-1997

C;Accession: B49164

R;Nielsen, E.; Welinder, B.S.; Madsen, O.D.

Endocrinology 129, 3147-3156, 1991

A;Title: Chromogranin-B, a putative precursor of eight novel rat glucagonoma peptides through processing at mono-, di-, or tribasic residues.

A;Reference number: A49164; MUID:92063871; PMID:1954895

A;Accession: B49164

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-11 <NIE>

A;Note: sequence extracted from NCBI backbone (NCBIP:66370)

C;Superfamily: chromogranin B precursor

Query Match 9.1%; Score 1; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 E 2  
|  
Db 4 E 4

RESULT 66

JN0023

substance P - chicken

C;Species: Gallus gallus (chicken)

C;Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 11-Jul-1997

C;Accession: JN0023

R;Conlon, J.M.; Katsoulis, S.; Schmidt, W.E.; Thim, L.

Regul. Pept. 20, 171-180, 1988

A;Title: [Arg3]substance P and neurokinin A from chicken small intestine.  
A;Reference number: JN0023; MUID:88204263; PMID:2452461  
A;Accession: JN0023  
A;Molecule type: protein  
A;Residues: 1-11 <CON>  
C;Superfamily: substance P precursor  
C;Keywords: amidated carboxyl end; tachykinin  
F;11/Modified site: amidated carboxyl end (Met) #status predicted

Query Match 9.1%; Score 1; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 G 3  
|  
Db 9 G 9

RESULT 67

S32575

ribosomal protein S2, plastid - squawroot plastid (fragment)

C;Species: plastid Conopholis americana (squawroot)

C;Date: 19-Mar-1997 #sequence\_revision 25-Apr-1997 #text\_change 13-Aug-1999

C;Accession: S32575

R;Taylor, G.W.; Wolfe, K.H.; Morden, C.W.; dePamphilis, C.W.; Palmer, J.D.  
Curr. Genet. 20, 515-518, 1991

A;Title: Lack of a functional plastid tRNA(Cys) gene is associated with loss of  
photosynthesis in a lineage of parasitic plants.

A;Reference number: S32575; MUID:92145776; PMID:1723664

A;Accession: S32575

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-11 <TAY>

A;Cross-references: EMBL:X64567; NID:g11275; PIDN:CAA45868.1; PID:g11276

C;Genetics:

A;Gene: rps2

A;Genome: plastid

C;Superfamily: Escherichia coli ribosomal protein S2

C;Keywords: plastid; protein biosynthesis; ribosome

Query Match 9.1%; Score 1; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 E 2  
|  
Db 11 E 11

RESULT 68

A40693

transgelin - sheep (fragment)

C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C;Date: 03-May-1994 #sequence\_revision 03-May-1994 #text\_change 31-Oct-1997

C;Accession: A40693

R;Shapland, C.; Hsuan, J.J.; Totty, N.F.; Lawson, D.  
J. Cell Biol. 121, 1065-1073, 1993

A;Title: Purification and properties of transgelin: a transformation and shape change sensitive actin-gelling protein.  
A;Reference number: A40693; MUID:93273790; PMID:8501116  
A;Accession: A40693  
A;Molecule type: protein  
A;Residues: 1-11 <SHA>  
A;Experimental source: aorta  
C;Comment: This protein gels actin and is down regulated by transformation or loss of cell adherence in culture.  
C;Superfamily: smooth muscle protein SM22; calponin repeat homology; smooth muscle protein SM22 homology  
C;Keywords: actin binding; cytoskeleton

Query Match 9.1%; Score 1; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 K 5  
|  
Db 1 K 1

RESULT 69

A38841  
rhodopsin homolog - squid (*Watasenia scintillans*) (fragment)  
N;Alternate names: visual pigment protein  
C;Species: *Watasenia scintillans* (sparkling enope)  
C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 31-Oct-1997  
C;Accession: A38841  
R;Seidou, M.; Kubota, I.; Hiraki, K.; Kito, Y.  
Biochim. Biophys. Acta 957, 318-321, 1988  
A;Title: Amino acid sequence of the retinal binding site of squid visual pigment.  
A;Reference number: PT0063; MUID:89051045; PMID:3191148  
A;Accession: A38841  
A;Molecule type: protein  
A;Residues: 1-11 <SEI>  
C;Superfamily: vertebrate rhodopsin  
C;Keywords: chromoprotein; retinal  
F;3/Binding site: retinal (Lys) (covalent) #status experimental

Query Match 9.1%; Score 1; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1  
|  
Db 2 A 2

RESULT 70

S00616  
parasporal crystal protein, wax moth-specific - *Bacillus thuringiensis* (strain galleriae 11-67) (fragment)  
N;Alternate names: delta-endotoxin; parasporal crystal protein positive chain  
C;Species: *Bacillus thuringiensis*  
C;Date: 31-Dec-1988 #sequence\_revision 31-Dec-1988 #text\_change 13-Sep-1996



C;Accession: S00616  
 R;Chestukhina, G.G.; Kostina, L.I.; Zalunin, I.A.; Khodova, O.M.; Stepanov, V.M.  
 FEBS Lett. 232, 249-251, 1988  
 A;Title: *Bacillus thuringiensis* ssp. *galleriae* simultaneously produces two  
 delta-endotoxins differing strongly in primary structure and entomocidal  
 activity.  
 A;Reference number: S00615  
 A;Accession: S00616  
 A;Molecule type: protein  
 A;Residues: 1-11 <CHE>  
 C;Comment: This toxin is effective against the larvae of *Galleria melonella*  
 (greater wax moth) but not those of *Lymantria dispar* (gypsy moth).  
 C;Superfamily: parasporal crystal protein  
 C;Keywords: delta-endotoxin

Query Match 9.1%; Score 1; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 2e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1  
 |  
 Db 4 A 4

# RESULT 71

S09074  
 cytochrome P450-4b - rat (fragment)  
 N;Alternate names: cytochrome P450K-5  
 N;Contains: oxidoreductase (EC 1.-.-.-)  
 C;Species: *Rattus norvegicus* (Norway rat)  
 C;Date: 23-Apr-1993 #sequence\_revision 23-Apr-1993 #text\_change 05-Mar-1999  
 C;Accession: S09074  
 R;Imaoka, S.; Terano, Y.; Funae, Y.  
 Arch. Biochem. Biophys. 278, 168-178, 1990  
 A;Title: Changes in the amount of cytochrome P450s in rat hepatic microsomes  
 with starvation.  
 A;Reference number: S09072; MUID:90210577; PMID:2321956  
 A;Accession: S09074  
 A;Molecule type: protein  
 A;Residues: 1-11 <IMA>  
 C;Superfamily: unassigned cytochrome P450; cytochrome P450 homology  
 C;Keywords: heme; microsome; monooxygenase; oxidoreductase; transmembrane  
 protein

Query Match 9.1%; Score 1; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 2e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 G 3  
 |  
 Db 10 G 10

# RESULT 72

A57458  
 gene Gax protein - mouse (fragment)  
 C;Species: *Mus* sp. (mouse)

C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 15-Oct-1999  
C;Accession: A57458  
R;Andres, V.; Fisher, S.; Wearsch, P.; Walsh, K.  
Mol. Cell. Biol. 15, 4272-4281, 1995  
A;Title: Regulation of Gax homeobox gene transcription by a combination of  
positive factors including myocyte-specific enhancer factor 2.  
A;Reference number: A57458; MUID:95349593; PMID:7623821  
A;Accession: A57458  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-11 <RES>  
A;Cross-references: GB:S79168; NID:g1050991  
C;Genetics:  
A;Gene: Gax  
C;Superfamily: unassigned homeobox proteins; homeobox homology  
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation

Query Match 9.1%; Score 1; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 M 9  
|  
Db 1 M 1

#### RESULT 73

A26930

ermG leader peptide 1 - Bacillus sphaericus

C;Species: Bacillus sphaericus

C;Date: 08-Mar-1989 #sequence\_revision 08-Mar-1989 #text\_change 24-Sep-1999

C;Accession: A26930

R;Monod, M.; Mohan, S.; Dubnau, D.

J. Bacteriol. 169, 340-350, 1987

A;Title: Cloning and analysis of ermG, a new macrolide-lincosamide-streptogramin  
B resistance element from Bacillus sphaericus.

A;Reference number: A91840; MUID:87083389; PMID:3025178

A;Accession: A26930

A;Molecule type: DNA

A;Residues: 1-11 <MON>

A;Cross-references: GB:M15332; NID:g142881; PIDN:AAA22417.1; PID:g142882

C;Superfamily: unassigned leader peptides

Query Match 9.1%; Score 1; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 M 9  
|  
Db 1 M 1

#### RESULT 74

D60409

kassinin-like peptide K-III - frog (Pseudophryne guentheri)

C;Species: Pseudophryne guentheri

C;Date: 30-Jan-1993 #sequence\_revision 30-Jan-1993 #text\_change 02-Sep-2000

C;Accession: D60409  
 R;Simmaco, M.; Severini, C.; De Biase, D.; Barra, D.; Bossa, F.; Roberts, J.D.;  
 Melchiorri, P.; Erspamer, V.  
 Peptides 11, 299-304, 1990  
 A;Title: Six novel tachykinin- and bombesin-related peptides from the skin of  
 the Australian frog *Pseudophryne guentheri*.  
 A;Reference number: A60409; MUID:90287814; PMID:2356157  
 A;Accession: D60409  
 A;Molecule type: protein  
 A;Residues: 1-11 <SIM>  
 C;Superfamily: unassigned animal peptides  
 C;Keywords: amidated carboxyl end; pyroglutamic acid  
 F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
 F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 9.1%; Score 1; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 2e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 E 2  
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 Db 6 E 6

#### RESULT 75

F60409  
 substance P-like peptide II - frog (*Pseudophryne guentheri*)  
 C;Species: *Pseudophryne guentheri*  
 C;Date: 30-Jan-1993 #sequence\_revision 30-Jan-1993 #text\_change 02-Sep-2000  
 C;Accession: F60409  
 R;Simmaco, M.; Severini, C.; De Biase, D.; Barra, D.; Bossa, F.; Roberts, J.D.;  
 Melchiorri, P.; Erspamer, V.  
 Peptides 11, 299-304, 1990  
 A;Title: Six novel tachykinin- and bombesin-related peptides from the skin of  
 the Australian frog *Pseudophryne guentheri*.  
 A;Reference number: A60409; MUID:90287814; PMID:2356157  
 A;Accession: F60409  
 A;Molecule type: protein  
 A;Residues: 1-11 <SIM>  
 C;Superfamily: unassigned animal peptides  
 C;Keywords: amidated carboxyl end; pyroglutamic acid  
 F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
 F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 9.1%; Score 1; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 2e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 E 2  
 |  
 Db 6 E 6

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 Job time : 9.61538 secs

OM protein - protein search, using sw model

Run on: April 8, 2004, 15:47:33 ; Search time 30.3077 Seconds  
(without alignments)  
95.432 Million cell updates/sec

Title: US-09-787-443A-19  
Perfect score: 11  
Sequence: 1 AEGGKKKKMRA 11

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 1073127 seqs, 262937947 residues

Word size : 0

Total number of hits satisfying chosen parameters: 9223

Minimum DB seq length: 11  
Maximum DB seq length: 11

Post-processing: Listing first 100 summaries

Database : Published Applications\_AA:\*  
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18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

8

Result	Query					
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2	5	45.5	11	10	US-09-876-904A-363	Sequence 363, App
3	4	36.4	11	9	US-09-846-342-1	Sequence 1, Appli
4	4	36.4	11	9	US-09-805-301-5	Sequence 5, Appli
5	4	36.4	11	9	US-09-805-301-43	Sequence 43, Appl
6	4	36.4	11	9	US-09-805-301-99	Sequence 99, Appl
7	4	36.4	11	10	US-09-882-291-55	Sequence 55, Appl
8	4	36.4	11	10	US-09-882-291-64	Sequence 64, Appl
9	4	36.4	11	10	US-09-876-904A-364	Sequence 364, App
10	4	36.4	11	10	US-09-791-524-15	Sequence 15, Appl
11	4	36.4	11	11	US-09-077-439A-16	Sequence 16, Appl
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14	4	36.4	11	14	US-10-212-499-39	Sequence 39, Appl
15	4	36.4	11	14	US-10-350-258-7	Sequence 7, Appli
16	4	36.4	11	14	US-10-355-975-33	Sequence 33, Appl
17	4	36.4	11	14	US-10-082-014-94	Sequence 94, Appl
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19	4	36.4	11	15	US-10-359-363A-46	Sequence 46, Appl
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22	4	36.4	11	15	US-10-359-363A-49	Sequence 49, Appl
23	4	36.4	11	15	US-10-359-363A-54	Sequence 54, Appl
24	4	36.4	11	15	US-10-359-363A-55	Sequence 55, Appl
25	4	36.4	11	15	US-10-359-363A-96	Sequence 96, Appl
26	4	36.4	11	15	US-10-359-363A-97	Sequence 97, Appl
27	4	36.4	11	15	US-10-359-363A-100	Sequence 100, App
28	3	27.3	11	9	US-09-828-592-10	Sequence 10, Appl
29	3	27.3	11	9	US-09-765-527-206	Sequence 206, App
30	3	27.3	11	9	US-09-010-714-5	Sequence 5, Appli
31	3	27.3	11	9	US-09-811-672-24	Sequence 24, Appl
32	3	27.3	11	9	US-09-845-667-1	Sequence 1, Appli
33	3	27.3	11	9	US-09-873-676-6	Sequence 6, Appli
34	3	27.3	11	9	US-09-873-676-19	Sequence 19, Appl
35	3	27.3	11	9	US-09-881-490-181	Sequence 181, App
36	3	27.3	11	9	US-09-977-831-32	Sequence 32, Appl
37	3	27.3	11	9	US-09-966-871-37	Sequence 37, Appl
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41	3	27.3	11	9	US-09-781-988-17	Sequence 17, Appl
42	3	27.3	11	9	US-09-969-192-19	Sequence 19, Appl
43	3	27.3	11	9	US-09-071-838-253	Sequence 253, App
44	3	27.3	11	9	US-09-823-823-36	Sequence 36, Appl
45	3	27.3	11	9	US-09-823-823-37	Sequence 37, Appl
46	3	27.3	11	9	US-09-965-967-26	Sequence 26, Appl
47	3	27.3	11	10	US-09-999-724-76	Sequence 76, Appl
48	3	27.3	11	10	US-09-931-325A-131	Sequence 131, App
49	3	27.3	11	10	US-09-931-325A-158	Sequence 158, App
50	3	27.3	11	10	US-09-876-904A-25	Sequence 25, Appl
51	3	27.3	11	10	US-09-876-904A-77	Sequence 77, Appl
52	3	27.3	11	10	US-09-876-904A-273	Sequence 273, App
53	3	27.3	11	10	US-09-876-904A-354	Sequence 354, App
54	3	27.3	11	10	US-09-876-904A-373	Sequence 373, App
55	3	27.3	11	10	US-09-876-904A-544	Sequence 544, App
56	3	27.3	11	10	US-09-876-904A-597	Sequence 597, App

57	3	27.3	11	10	US-09-852-910-238	Sequence 238, App
58	3	27.3	11	10	US-09-972-656-7	Sequence 7, Appli
59	3	27.3	11	10	US-09-893-878-17	Sequence 17, Appl
60	3	27.3	11	10	US-09-930-915A-172	Sequence 172, App
61	3	27.3	11	10	US-09-930-915A-195	Sequence 195, App
62	3	27.3	11	10	US-09-933-767-1184	Sequence 1184, Ap
63	3	27.3	11	11	US-09-896-095-17	Sequence 17, Appl
64	3	27.3	11	12	US-10-361-270-18	Sequence 18, Appl
65	3	27.3	11	12	US-10-458-860-37	Sequence 37, Appl
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67	3	27.3	11	12	US-10-601-837-222	Sequence 222, App
68	3	27.3	11	12	US-10-668-400-17	Sequence 17, Appl
69	3	27.3	11	12	US-10-668-400-18	Sequence 18, Appl
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73	3	27.3	11	14	US-10-108-795-26	Sequence 26, Appl
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79	3	27.3	11	14	US-10-115-365-29	Sequence 29, Appl
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83	3	27.3	11	14	US-10-023-282-1184	Sequence 1184, Ap
84	3	27.3	11	14	US-10-044-692-98	Sequence 98, Appl
85	3	27.3	11	14	US-10-044-539-98	Sequence 98, Appl
86	3	27.3	11	14	US-10-149-326-12	Sequence 12, Appl
87	3	27.3	11	14	US-10-213-512-253	Sequence 253, App
88	3	27.3	11	14	US-10-174-613-46	Sequence 46, Appl
89	3	27.3	11	14	US-10-251-364-12	Sequence 12, Appl
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91	3	27.3	11	14	US-10-148-786A-14	Sequence 14, Appl
92	3	27.3	11	14	US-10-283-423-126	Sequence 126, App
93	3	27.3	11	14	US-10-072-419-37	Sequence 37, Appl
94	3	27.3	11	14	US-10-116-212-26	Sequence 26, Appl
95	3	27.3	11	14	US-10-116-212-29	Sequence 29, Appl
96	3	27.3	11	14	US-10-286-457-349	Sequence 349, App
97	3	27.3	11	14	US-10-286-457-634	Sequence 634, App
98	3	27.3	11	14	US-10-161-660-29	Sequence 29, Appl
99	3	27.3	11	14	US-10-020-269-34	Sequence 34, Appl
100	3	27.3	11	14	US-10-213-821-126	Sequence 126, App

#### ALIGNMENTS

##### RESULT 1

US-09-876-904A-362

; Sequence 362, Application US/09876904A

; Publication No. US20030072794A1

; GENERAL INFORMATION:

; APPLICANT: BOULIKAS, TENI

; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND  
THERAPEUTIC

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; TITLE OF INVENTION:  AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC
PEPTIDE
; TITLE OF INVENTION:  CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
; FILE REFERENCE: TB-2002.00
; CURRENT APPLICATION NUMBER: US/09/876,904A
; CURRENT FILING DATE:  2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,925
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 629
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 362
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Mus sp.
; FEATURE:
; OTHER INFORMATION: Murine LEF-1.
US-09-876-904A-362
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Query Match          45.5%;  Score 5;  DB 10;  Length 11;
Best Local Similarity 100.0%;  Pred. No. 1.4e+02;
Matches      5;  Conservative    0;  Mismatches    0;  Indels      0;  Gaps      0;
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Qy          4 GKKKK 8
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Db          1 GKKKK 5
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## RESULT 2

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US-09-876-904A-363
; Sequence 363, Application US/09876904A
; Publication No. US20030072794A1
; GENERAL INFORMATION:
; APPLICANT: BOULIKAS, TENI
; TITLE OF INVENTION:  ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND
THERAPEUTIC
; TITLE OF INVENTION:  AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC
PEPTIDE
; TITLE OF INVENTION:  CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
; FILE REFERENCE: TB-2002.00
; CURRENT APPLICATION NUMBER: US/09/876,904A
; CURRENT FILING DATE:  2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,925
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 629
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 363
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Human TCF-1 alpha.
US-09-876-904A-363
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Query Match          45.5%;  Score 5;  DB 10;  Length 11;
Best Local Similarity 100.0%;  Pred. No. 1.4e+02;
Matches      5;  Conservative    0;  Mismatches    0;  Indels      0;  Gaps      0;
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Qy 4 GKKKK 8  
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Db 1 GKKKK 5

RESULT 3

US-09-846-342-1

; Sequence 1, Application US/09846342

; Patent No. US20020160422A1

; GENERAL INFORMATION:

; APPLICANT: Jackowski, George

; TITLE OF INVENTION: BIOPOLYMER MARKER INDICATIVE OF DISEASE STATE HAVING A  
MOLECULAR WEIGHT

; TITLE OF INVENTION: OF 1077 DALTONS

; FILE REFERENCE: 2132.026

; CURRENT APPLICATION NUMBER: US/09/846,342

; CURRENT FILING DATE: 2001-04-30

; NUMBER OF SEQ ID NOS: 1

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 1

; LENGTH: 11

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-846-342-1

Query Match 36.4%; Score 4; DB 9; Length 11;

Best Local Similarity 100.0%; Pred. No. 1.3e+03;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEGG 4  
|||||  
Db 5 AEGG 8

RESULT 4

US-09-805-301-5

; Sequence 5, Application US/09805301

; Patent No. US20020173456A1

; GENERAL INFORMATION:

; APPLICANT: Smith, Louis C.

; Sparrow, James T.

; Hauer, Jochen

; Mims, Martha P.

; TITLE OF INVENTION: LIPOPHILIC PEPTIDES FOR  
MACROMOLECULE DELIVERY

; NUMBER OF SEQUENCES: 139

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon & Lyon

; STREET: 633 West Fifth Street

; Suite 4700

; CITY: Los Angeles

; STATE: California

; COUNTRY: U.S.A.

; ZIP: 90071-2066

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
storage



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;      COMPUTER: IBM Compatible
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;      APPLICATION NUMBER: US/09/805,301
;      FILING DATE: 12-Mar-2001
;      CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: 08/584,043
;      FILING DATE: <Unknown>
;
; ATTORNEY/AGENT INFORMATION:
;      NAME: Warburg, Richard J.
;      REGISTRATION NUMBER: 32,327
;      REFERENCE/DOCKET NUMBER: 217/189
;
; TELECOMMUNICATION INFORMATION:
;      TELEPHONE: (213) 489-1600
;      TELEFAX: (213) 955-0440
;      TELEX: 67-3510
;
; INFORMATION FOR SEQ ID NO: 5:
;      SEQUENCE CHARACTERISTICS:
;          LENGTH: 11 amino acids
;          TYPE: amino acid
;          STRANDEDNESS: single
;          TOPOLOGY: linear
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;      MOLECULE TYPE: peptide
;      SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-805-301-5

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Query Match          36.4%;  Score 4;  DB 9;  Length 11;
Best Local Similarity 100.0%;  Pred. No. 1.3e+03;
Matches      4;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

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Qy      5 KKKK 8
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Db      1 KKKK 4

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# RESULT 5

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US-09-805-301-43
; Sequence 43, Application US/09805301
; Patent No. US20020173456A1
;   GENERAL INFORMATION:
;       APPLICANT: Smith, Louis C.
;               Sparrow, James T.
;               Hauer, Jochen
;               Mims, Martha P.
;
;   TITLE OF INVENTION: LIPOPHILIC PEPTIDES FOR
;                       MACROMOLECULE DELIVERY
;
;   NUMBER OF SEQUENCES: 139
;   CORRESPONDENCE ADDRESS:
;       ADDRESSEE: Lyon & Lyon
;       STREET: 633 West Fifth Street
;               Suite 4700
;       CITY: Los Angeles
;       STATE: California
;       COUNTRY: U.S.A.
;       ZIP: 90071-2066

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;      COMPUTER READABLE FORM:
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;      OPERATING SYSTEM: IBM P.C. DOS 6.0
;      SOFTWARE: Word Perfect 6.1
;      CURRENT APPLICATION DATA:
;      APPLICATION NUMBER: US/09/805,301
;      FILING DATE: 12-Mar-2001
;      CLASSIFICATION: <Unknown>
;      PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: 08/584,043
;      FILING DATE: <Unknown>
;      ATTORNEY/AGENT INFORMATION:
;      NAME: Warburg, Richard J.
;      REGISTRATION NUMBER: 32,327
;      REFERENCE/DOCKET NUMBER: 217/189
;      TELECOMMUNICATION INFORMATION:
;      TELEPHONE: (213) 489-1600
;      TELEFAX: (213) 955-0440
;      TELEX: 67-3510
;      INFORMATION FOR SEQ ID NO: 43:
;      SEQUENCE CHARACTERISTICS:
;      LENGTH: 11 amino acids
;      TYPE: amino acid
;      STRANDEDNESS: single
;      TOPOLOGY: linear
;      MOLECULE TYPE: peptide
;      FEATURE:
;      OTHER INFORMATION:      "Xaa" stands for any naturally
;      occurring amino acid and
;      analogues thereof.
;      SEQUENCE DESCRIPTION: SEQ ID NO: 43:
US-09-805-301-43

```

```

Query Match          36.4%;  Score 4;  DB 9;  Length 11;
Best Local Similarity 100.0%;  Pred. No. 1.3e+03;
Matches      4;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

```

```

Qy      5 KKKK 8
        ||||
Db      1 KKKK 4

```

# RESULT 6

```

US-09-805-301-99
; Sequence 99, Application US/09805301
; Patent No. US20020173456A1
;      GENERAL INFORMATION:
;      APPLICANT: Smith, Louis C.
;      Sparrow, James T.
;      Hauer, Jochen
;      Mims, Martha P.
;      TITLE OF INVENTION: LIPOPHILIC PEPTIDES FOR
;      MACROMOLECULE DELIVERY
;      NUMBER OF SEQUENCES: 139
;      CORRESPONDENCE ADDRESS:

```

```

;      ADDRESSEE: Lyon & Lyon
;      STREET: 633 West Fifth Street
;             Suite 4700
;      CITY: Los Angeles
;      STATE: California
;      COUNTRY: U.S.A.
;      ZIP: 90071-2066
;      COMPUTER READABLE FORM:
;             MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
;                     storage
;      COMPUTER: IBM Compatible
;      OPERATING SYSTEM: IBM P.C. DOS 6.0
;      SOFTWARE: Word Perfect 6.1
;      CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/805,301
;             FILING DATE: 12-Mar-2001
;             CLASSIFICATION: <Unknown>
;      PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/584,043
;             FILING DATE: <Unknown>
;      ATTORNEY/AGENT INFORMATION:
;             NAME: Warburg, Richard J.
;             REGISTRATION NUMBER: 32,327
;             REFERENCE/DOCKET NUMBER: 217/189
;      TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (213) 489-1600
;             TELEFAX: (213) 955-0440
;             TELEX: 67-3510
;      INFORMATION FOR SEQ ID NO: 99:
;      SEQUENCE CHARACTERISTICS:
;             LENGTH: 11 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;      MOLECULE TYPE: peptide
;      SEQUENCE DESCRIPTION: SEQ ID NO: 99:
US-09-805-301-99

```

```

Query Match          36.4%; Score 4; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches      4; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      5 KKKK 8
        ||||
Db      1 KKKK 4

```

# RESULT 7

```

US-09-882-291-55
; Sequence 55, Application US/09882291
; Publication No. US20030040472A1
; GENERAL INFORMATION:
; APPLICANT: Zealand Pharmaceuticals A/S
; TITLE OF INVENTION: No. US20030040472A1e1 Peptide Conjugates
; FILE REFERENCE: 007-2001
; CURRENT APPLICATION NUMBER: US/09/882,291
; CURRENT FILING DATE: 2001-06-15

```

; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 55  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic peptide  
sequence  
US-09-882-291-55

Query Match 36.4%; Score 4; DB 10; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KKKK 8  
| | | |  
Db 6 KKKK 9

RESULT 8  
US-09-882-291-64  
; Sequence 64, Application US/09882291  
; Publication No. US20030040472A1  
; GENERAL INFORMATION:  
; APPLICANT: Zealand Pharmaceuticals A/S  
; TITLE OF INVENTION: No. US20030040472A1e1 Peptide Conjugates  
; FILE REFERENCE: 007-2001  
; CURRENT APPLICATION NUMBER: US/09/882,291  
; CURRENT FILING DATE: 2001-06-15  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 64  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic peptide  
sequence  
US-09-882-291-64

Query Match 36.4%; Score 4; DB 10; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KKKK 8  
| | | |  
Db 6 KKKK 9

RESULT 9  
US-09-876-904A-364  
; Sequence 364, Application US/09876904A  
; Publication No. US20030072794A1  
; GENERAL INFORMATION:  
; APPLICANT: BOULIKAS, TENI

```
; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND
THERAPEUTIC
; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC
PEPTIDE
; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
; FILE REFERENCE: TB-2002.00
; CURRENT APPLICATION NUMBER: US/09/876,904A
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,925
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 629
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 364
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Human TCF-1
US-09-876-904A-364
```

```
Query Match          36.4%; Score 4; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches      4; Conservative      0; Mismatches      0; Indels      0; Gaps      0;
```

```
Qy      4 GKKK 7
        ||||
Db      1 GKKK 4
```

```
RESULT 10
US-09-791-524-15
; Sequence 15, Application US/09791524
; Publication No. US20030143209A1
; GENERAL INFORMATION:
; APPLICANT: Aventis Pharmaceuticals Products Inc.
; TITLE OF INVENTION: Targeted Adenovirus Vectors For Delivery Of
Heterologous Genes
; FILE REFERENCE: A3319A
; CURRENT APPLICATION NUMBER: US/09/791,524
; CURRENT FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/09828
; PRIOR FILING DATE: 1998-08-27
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 15
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Adenovirus
US-09-791-524-15
```

```
Query Match          36.4%; Score 4; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches      4; Conservative      0; Mismatches      0; Indels      0; Gaps      0;
```

```
Qy      5 KKKK 8
        ||||
Db      3 KKKK 6
```

RESULT 11

US-09-077-439A-16

; Sequence 16, Application US/09077439A  
 ; Publication No. US20030202989A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Collier, R. John  
 ; APPLICANT: Blanke, Steven R.  
 ; APPLICANT: Milne, Jill C.  
 ; APPLICANT: Benson, Ericka L.  
 ; APPLICANT: Ballard, Jimmy D.  
 ; APPLICANT: Starnbach, Michael N.  
 ; TITLE OF INVENTION: Use of Toxin Peptides and/or Affinity  
 ; TITLE OF INVENTION: Handles for Delivering Compounds into Cells  
 ; FILE REFERENCE: 00246/187002  
 ; CURRENT APPLICATION NUMBER: US/09/077,439A  
 ; CURRENT FILING DATE: 1999-04-08  
 ; PRIOR APPLICATION NUMBER: PCT/US96/20463  
 ; PRIOR FILING DATE: 1996-12-13  
 ; PRIOR APPLICATION NUMBER: US 60/019,275  
 ; PRIOR FILING DATE: 1996-06-07  
 ; PRIOR APPLICATION NUMBER: US 60/008,518  
 ; PRIOR FILING DATE: 1995-12-13  
 ; NUMBER OF SEQ ID NOS: 26  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO 16  
 ; LENGTH: 11  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Synthetic Protein  
 US-09-077-439A-16

Query Match 36.4%; Score 4; DB 11; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KKKK 8  
 ||||  
 Db 1 KKKK 4

RESULT 12

US-10-156-527-5

; Sequence 5, Application US/10156527  
 ; Publication No. US20040063628A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: PICCARIELLO, THOMAS  
 ; APPLICANT: KIRK, RANDAL  
 ; APPLICANT: OLON, LAWRENCE  
 ; TITLE OF INVENTION: ACTIVE AGENT DELIVERY SYSTEMS AND METHODS FOR PROTECTING  
 AND  
 ; TITLE OF INVENTION: ADMINISTERING ACTIVE AGENTS  
 ; FILE REFERENCE: 54719.000063  
 ; CURRENT APPLICATION NUMBER: US/10/156,527  
 ; CURRENT FILING DATE: 2002-05-29

; PRIOR APPLICATION NUMBER: 09/986,426  
 ; PRIOR FILING DATE: 2001-11-08  
 ; PRIOR APPLICATION NUMBER: 09/411,238  
 ; PRIOR FILING DATE: 1999-10-04  
 ; PRIOR APPLICATION NUMBER: 09/265,415  
 ; PRIOR FILING DATE: 1999-03-10  
 ; PRIOR APPLICATION NUMBER: 09/642,820  
 ; PRIOR FILING DATE: 2000-08-22  
 ; PRIOR APPLICATION NUMBER: 09/987,458  
 ; PRIOR FILING DATE: 2001-11-14  
 ; PRIOR APPLICATION NUMBER: 09/988,071  
 ; PRIOR FILING DATE: 2001-11-16  
 ; PRIOR APPLICATION NUMBER: 09/988,034  
 ; PRIOR FILING DATE: 2001-11-16  
 ; PRIOR APPLICATION NUMBER: 09/933,708  
 ; PRIOR FILING DATE: 2001-08-22  
 ; PRIOR APPLICATION NUMBER: PCT/US01/43089  
 ; PRIOR FILING DATE: 2001-11-14  
 ; PRIOR APPLICATION NUMBER: PCT/US01/43117  
 ; PRIOR FILING DATE: 2001-11-16  
 ; Remaining Prior Application data removed - See File Wrapper or PALM.  
 ; NUMBER OF SEQ ID NOS: 23  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 5  
 ; LENGTH: 11  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 ; OTHER INFORMATION: peptide  
 US-10-156-527-5

Query Match 36.4%; Score 4; DB 12; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KKKK 8  
 ||||  
 Db 1 KKKK 4

# RESULT 13

US-10-156-527-12

; Sequence 12, Application US/10156527  
 ; Publication No. US20040063628A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: PICCARIELLO, THOMAS  
 ; APPLICANT: KIRK, RANDAL  
 ; APPLICANT: OLON, LAWRENCE  
 ; TITLE OF INVENTION: ACTIVE AGENT DELIVERY SYSTEMS AND METHODS FOR PROTECTING  
 AND  
 ; TITLE OF INVENTION: ADMINISTERING ACTIVE AGENTS  
 ; FILE REFERENCE: 54719.000063  
 ; CURRENT APPLICATION NUMBER: US/10/156,527  
 ; CURRENT FILING DATE: 2002-05-29  
 ; PRIOR APPLICATION NUMBER: 09/986,426  
 ; PRIOR FILING DATE: 2001-11-08

```

; PRIOR APPLICATION NUMBER: 09/411,238
; PRIOR FILING DATE: 1999-10-04
; PRIOR APPLICATION NUMBER: 09/265,415
; PRIOR FILING DATE: 1999-03-10
; PRIOR APPLICATION NUMBER: 09/642,820
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 09/987,458
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 09/988,071
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 09/988,034
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 09/933,708
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: PCT/US01/43089
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: PCT/US01/43117
; PRIOR FILING DATE: 2001-11-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
;   LENGTH: 11
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: peptide
;   FEATURE:
;   OTHER INFORMATION: this peptide may encompass 4-11 residues according to the
;   OTHER INFORMATION: specification as filed
US-10-156-527-12

```

```

Query Match          36.4%; Score 4; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches      4; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy          5 KKKK 8
             ||||
Db          1 KKKK 4

```

#### RESULT 14

US-10-212-499-39

```

; Sequence 39, Application US/10212499
; Publication No. US20030135036A1
;   GENERAL INFORMATION:
;       APPLICANT: Lanza, Francois
;               Phillips, David R.
;               Cazenave, Jean-Pierre
;   TITLE OF INVENTION: Platelet Glycoprotein V Gene and Uses
;   NUMBER OF SEQUENCES: 43
;   CORRESPONDENCE ADDRESS:
;       ADDRESSEE: Morgan Lewis & Bockius LLP
;       STREET: 1800 M St., NW
;       CITY: Washington
;       STATE: DC

```



```

;          COUNTRY: US
;          ZIP: 20036
;
;  COMPUTER READABLE FORM:
;          MEDIUM TYPE: Floppy disk
;          COMPUTER: IBM PC compatible
;          OPERATING SYSTEM: PC-DOS/MS-DOS
;
;  CURRENT APPLICATION DATA:
;          APPLICATION NUMBER: US/10/212,499
;          FILING DATE: 06-Aug-2002
;
;  PRIOR APPLICATION DATA:
;          APPLICATION NUMBER: US/09/560,814
;          FILING DATE: 2000-04-28
;          APPLICATION NUMBER: US 08/089,455
;          FILING DATE: 1993-07-09
;          APPLICATION NUMBER: US 08/195,006
;          FILING DATE: 1994-02-10
;          APPLICATION NUMBER: US 08/884,571
;          FILING DATE: 1997-06-27
;
;  ATTORNEY/AGENT INFORMATION:
;          NAME: Reid G. Adler
;          REGISTRATION NUMBER: 30,988
;          REFERENCE/DOCKET NUMBER: 44481-5018-04-US
;
;  TELECOMMUNICATION INFORMATION:
;          TELEPHONE: 202-467-7000
;          TELEFAX: 202-467-7176
;
;  INFORMATION FOR SEQ ID NO: 39:
;          SEQUENCE CHARACTERISTICS:
;              LENGTH: 11 amino acids
;              TYPE: amino acid
;              TOPOLOGY: unknown
;          MOLECULE TYPE: peptide
;          HYPOTHETICAL: NO
;          FEATURE:
;              NAME/KEY: Peptide
;              LOCATION: 1..11
;              OTHER INFORMATION: /note= "Amino acid sequence of the
;              human fibrinogen (Fg) A-alpha 1 chain thrombin
;              cleavage site."
;          FEATURE:
;              NAME/KEY: Region
;              LOCATION: 1..2
;              OTHER INFORMATION: /note= "Amino acid residues
;              identical to GPV."
;          FEATURE:
;              NAME/KEY: Region
;              LOCATION: 5
;              OTHER INFORMATION: /note= "Amino acid residue
;              identical to GPV."
;          FEATURE:
;              NAME/KEY: Region
;              LOCATION: 7..9
;              OTHER INFORMATION: /note= "Amino acid residues
;              identical to GPV."
;          SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-10-212-499-39

```

Query Match

36.4%; Score 4; DB 14; Length 11;

Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEGG 4  
||||  
Db 1 AEGG 4

RESULT 15

US-10-350-258-7  
; Sequence 7, Application US/10350258  
; Publication No. US20030139345A1  
; GENERAL INFORMATION:  
; APPLICANT: MATTHIAS RATH  
; TITLE OF INVENTION: SYNTHETIC PEPTIDES AND METHODS FOR TREATING CANCER  
INVASION AND METASTASIS  
; FILE REFERENCE: 11957/23  
; CURRENT APPLICATION NUMBER: US/10/350,258  
; CURRENT FILING DATE: 2003-01-22  
; PRIOR APPLICATION NUMBER: 60/351,317  
; PRIOR FILING DATE: January 23, 2002  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 7  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-350-258-7

Query Match 36.4%; Score 4; DB 14; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 KKKM 9  
||||  
Db 6 KKKM 9

RESULT 16

US-10-355-975-33  
; Sequence 33, Application US/10355975  
; Publication No. US20030162277A1  
; GENERAL INFORMATION:  
; APPLICANT: Immunex Corporation  
; APPLICANT: Bird, Timothy A.  
; APPLICANT: Virca, G. Duke  
; APPLICANT: Martin, Unja  
; APPLICANT: Anderson, Dirk M.  
; TITLE OF INVENTION: NOVEL MURINE AND HUMAN KINASES  
; FILE REFERENCE: 2923-A  
; CURRENT APPLICATION NUMBER: US/10/355,975  
; CURRENT FILING DATE: 2003-01-30  
; PRIOR APPLICATION NUMBER: US/09/579,664B  
; PRIOR FILING DATE: 2000-05-26  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 33

; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: peptide  
US-10-355-975-33

Query Match 36.4%; Score 4; DB 14; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KKKK 8  
||||  
Db 1 KKKK 4

RESULT 17

US-10-082-014-94  
; Sequence 94, Application US/10082014  
; Publication No. US20030185858A1  
; GENERAL INFORMATION:  
; APPLICANT: Birkett, Ashley J.  
; TITLE OF INVENTION: IMMUNOGENIC HbC CHIMER PARTICLES STABILIZED WITH AN N-  
TERMINAL CYSTEINE  
; FILE REFERENCE: ICC-130.0 4564/85124  
; CURRENT APPLICATION NUMBER: US/10/082,014  
; CURRENT FILING DATE: 2002-02-22  
; PRIOR APPLICATION NUMBER: 09/930,915  
; PRIOR FILING DATE: 2001-08-15  
; NUMBER OF SEQ ID NOS: 290  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 94  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-10-082-014-94

Query Match 36.4%; Score 4; DB 14; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 KKKM 9  
||||  
Db 5 KKKM 8

RESULT 18

US-10-372-076-95  
; Sequence 95, Application US/10372076  
; Publication No. US20030198645A1  
; GENERAL INFORMATION:  
; APPLICANT: Page, Mark  
; APPLICANT: Friede, Martin  
; TITLE OF INVENTION: STABILIZED HbC CHIMER PARTICLES AS THERAPEUTIC VACCINE  
FOR  
; TITLE OF INVENTION: CHRONIC HEPATITIS  
; FILE REFERENCE: 4564/87179

; CURRENT APPLICATION NUMBER: US/10/372,076  
; CURRENT FILING DATE: 2003-02-21  
; PRIOR APPLICATION NUMBER: 10/080,299  
; PRIOR FILING DATE: 2002-02-21  
; PRIOR APPLICATION NUMBER: 10/082,014  
; PRIOR FILING DATE: 2002-02-22  
; NUMBER OF SEQ ID NOS: 308  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 95  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-10-372-076-95

Query Match 36.4%; Score 4; DB 14; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 KKKM 9  
| | | |  
Db 5 KKKM 8

RESULT 19

US-10-359-363A-46

; Sequence 46, Application US/10359363A  
; Publication No. US20030228371A1  
; GENERAL INFORMATION:  
; APPLICANT: Skinner, James E.  
; APPLICANT: Anchin, Jerry M.  
; TITLE OF INVENTION: ANTI-INFARCTION MOLECULES  
; FILE REFERENCE: 22118.0001U4  
; CURRENT APPLICATION NUMBER: US/10/359,363A  
; CURRENT FILING DATE: 2003-02-05  
; PRIOR APPLICATION NUMBER: 60/429,278  
; PRIOR FILING DATE: 2002-11-25  
; PRIOR APPLICATION NUMBER: 60/392,133  
; PRIOR FILING DATE: 2002-06-28  
; PRIOR APPLICATION NUMBER: 60/354,678  
; PRIOR FILING DATE: 2002-02-06  
; NUMBER OF SEQ ID NOS: 104  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 46  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:/No. US20030228371A1e  
=  
; OTHER INFORMATION: Synthetic Construct  
US-10-359-363A-46

Query Match 36.4%; Score 4; DB 15; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEGG 4

Db                   |||||  
                    5 AEGG 8

RESULT 20

US-10-359-363A-47

; Sequence 47, Application US/10359363A  
; Publication No. US20030228371A1  
; GENERAL INFORMATION:  
; APPLICANT: Skinner, James E.  
; APPLICANT: Anchin, Jerry M.  
; TITLE OF INVENTION: ANTI-INFARCTION MOLECULES  
; FILE REFERENCE: 22118.0001U4  
; CURRENT APPLICATION NUMBER: US/10/359,363A  
; CURRENT FILING DATE: 2003-02-05  
; PRIOR APPLICATION NUMBER: 60/429,278  
; PRIOR FILING DATE: 2002-11-25  
; PRIOR APPLICATION NUMBER: 60/392,133  
; PRIOR FILING DATE: 2002-06-28  
; PRIOR APPLICATION NUMBER: 60/354,678  
; PRIOR FILING DATE: 2002-02-06  
; NUMBER OF SEQ ID NOS: 104  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 47  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:/No. US20030228371A1e  
=  
; OTHER INFORMATION: Synthetic Construct  
US-10-359-363A-47

Query Match                   36.4%; Score 4; DB 15; Length 11;  
Best Local Similarity   100.0%; Pred. No. 1.3e+03;  
Matches       4; Conservative       0; Mismatches       0; Indels       0; Gaps       0;

Qy                   1 AEGG 4  
                    |||||  
Db                   5 AEGG 8

RESULT 21

US-10-359-363A-48

; Sequence 48, Application US/10359363A  
; Publication No. US20030228371A1  
; GENERAL INFORMATION:  
; APPLICANT: Skinner, James E.  
; APPLICANT: Anchin, Jerry M.  
; TITLE OF INVENTION: ANTI-INFARCTION MOLECULES  
; FILE REFERENCE: 22118.0001U4  
; CURRENT APPLICATION NUMBER: US/10/359,363A  
; CURRENT FILING DATE: 2003-02-05  
; PRIOR APPLICATION NUMBER: 60/429,278  
; PRIOR FILING DATE: 2002-11-25  
; PRIOR APPLICATION NUMBER: 60/392,133  
; PRIOR FILING DATE: 2002-06-28

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; PRIOR APPLICATION NUMBER: 60/354,678
; PRIOR FILING DATE: 2002-02-06
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 48
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/No. US20030228371A1e
=
; OTHER INFORMATION: Synthetic Construct
US-10-359-363A-48

```

```

Query Match          36.4%; Score 4; DB 15; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches      4; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      1 AEGG 4
        ||||
Db      5 AEGG 8

```

# RESULT 22

US-10-359-363A-49

```

; Sequence 49, Application US/10359363A
; Publication No. US20030228371A1
; GENERAL INFORMATION:
; APPLICANT: Skinner, James E.
; APPLICANT: Anchin, Jerry M.
; TITLE OF INVENTION: ANTI-INFARCTION MOLECULES
; FILE REFERENCE: 22118.0001U4
; CURRENT APPLICATION NUMBER: US/10/359,363A
; CURRENT FILING DATE: 2003-02-05
; PRIOR APPLICATION NUMBER: 60/429,278
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/392,133
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: 60/354,678
; PRIOR FILING DATE: 2002-02-06
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 49
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/No. US20030228371A1e
=
; OTHER INFORMATION: Synthetic Construct
US-10-359-363A-49

```

```

Query Match          36.4%; Score 4; DB 15; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches      4; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      1 AEGG 4

```

Db           |||||  
              5 AEGG 8

RESULT 23

US-10-359-363A-54

; Sequence 54, Application US/10359363A  
; Publication No. US20030228371A1  
; GENERAL INFORMATION:  
; APPLICANT: Skinner, James E.  
; APPLICANT: Anchin, Jerry M.  
; TITLE OF INVENTION: ANTI-INFARCTION MOLECULES  
; FILE REFERENCE: 22118.0001U4  
; CURRENT APPLICATION NUMBER: US/10/359,363A  
; CURRENT FILING DATE: 2003-02-05  
; PRIOR APPLICATION NUMBER: 60/429,278  
; PRIOR FILING DATE: 2002-11-25  
; PRIOR APPLICATION NUMBER: 60/392,133  
; PRIOR FILING DATE: 2002-06-28  
; PRIOR APPLICATION NUMBER: 60/354,678  
; PRIOR FILING DATE: 2002-02-06  
; NUMBER OF SEQ ID NOS: 104  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 54  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:/No. US20030228371A1e  
=  
; OTHER INFORMATION: Synthetic Construct  
US-10-359-363A-54

Query Match                   36.4%; Score 4; DB 15; Length 11;  
Best Local Similarity   100.0%; Pred. No. 1.3e+03;  
Matches       4; Conservative   0; Mismatches    0; Indels       0; Gaps       0;

Qy           1 AEGG 4  
              |||||  
Db           5 AEGG 8

RESULT 24

US-10-359-363A-55

; Sequence 55, Application US/10359363A  
; Publication No. US20030228371A1  
; GENERAL INFORMATION:  
; APPLICANT: Skinner, James E.  
; APPLICANT: Anchin, Jerry M.  
; TITLE OF INVENTION: ANTI-INFARCTION MOLECULES  
; FILE REFERENCE: 22118.0001U4  
; CURRENT APPLICATION NUMBER: US/10/359,363A  
; CURRENT FILING DATE: 2003-02-05  
; PRIOR APPLICATION NUMBER: 60/429,278  
; PRIOR FILING DATE: 2002-11-25  
; PRIOR APPLICATION NUMBER: 60/392,133  
; PRIOR FILING DATE: 2002-06-28

```

; PRIOR APPLICATION NUMBER: 60/354,678
; PRIOR FILING DATE: 2002-02-06
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 55
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/No. US20030228371A1e
=
; OTHER INFORMATION: Synthetic Construct
US-10-359-363A-55

```

```

Query Match          36.4%; Score 4; DB 15; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches      4; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      1 AEGG 4
        ||||
Db      5 AEGG 8

```

# RESULT 25

```

US-10-359-363A-96
; Sequence 96, Application US/10359363A
; Publication No. US20030228371A1
; GENERAL INFORMATION:
; APPLICANT: Skinner, James E.
; APPLICANT: Anchin, Jerry M.
; TITLE OF INVENTION: ANTI-INFARCTION MOLECULES
; FILE REFERENCE: 22118.0001U4
; CURRENT APPLICATION NUMBER: US/10/359,363A
; CURRENT FILING DATE: 2003-02-05
; PRIOR APPLICATION NUMBER: 60/429,278
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/392,133
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: 60/354,678
; PRIOR FILING DATE: 2002-02-06
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 96
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/No. US20030228371A1e
=
; OTHER INFORMATION: Synthetic Construct
US-10-359-363A-96

```

```

Query Match          36.4%; Score 4; DB 15; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches      4; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      1 AEGG 4

```



Db            5 AEGG 8

RESULT 26

US-10-359-363A-97

; Sequence 97, Application US/10359363A  
; Publication No. US20030228371A1  
; GENERAL INFORMATION:  
; APPLICANT: Skinner, James E.  
; APPLICANT: Anchin, Jerry M.  
; TITLE OF INVENTION: ANTI-INFARCTION MOLECULES  
; FILE REFERENCE: 22118.0001U4  
; CURRENT APPLICATION NUMBER: US/10/359,363A  
; CURRENT FILING DATE: 2003-02-05  
; PRIOR APPLICATION NUMBER: 60/429,278  
; PRIOR FILING DATE: 2002-11-25  
; PRIOR APPLICATION NUMBER: 60/392,133  
; PRIOR FILING DATE: 2002-06-28  
; PRIOR APPLICATION NUMBER: 60/354,678  
; PRIOR FILING DATE: 2002-02-06  
; NUMBER OF SEQ ID NOS: 104  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 97  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:/No. US20030228371A1e  
=  
; OTHER INFORMATION: Synthetic Construct  
US-10-359-363A-97

Query Match            36.4%; Score 4; DB 15; Length 11;  
Best Local Similarity   100.0%; Pred. No. 1.3e+03;  
Matches        4; Conservative        0; Mismatches        0; Indels        0; Gaps        0;

Qy            1 AEGG 4  
              1111  
Db            5 AEGG 8

RESULT 27

US-10-359-363A-100

; Sequence 100, Application US/10359363A  
; Publication No. US20030228371A1  
; GENERAL INFORMATION:  
; APPLICANT: Skinner, James E.  
; APPLICANT: Anchin, Jerry M.  
; TITLE OF INVENTION: ANTI-INFARCTION MOLECULES  
; FILE REFERENCE: 22118.0001U4  
; CURRENT APPLICATION NUMBER: US/10/359,363A  
; CURRENT FILING DATE: 2003-02-05  
; PRIOR APPLICATION NUMBER: 60/429,278  
; PRIOR FILING DATE: 2002-11-25  
; PRIOR APPLICATION NUMBER: 60/392,133  
; PRIOR FILING DATE: 2002-06-28

; PRIOR APPLICATION NUMBER: 60/354,678  
; PRIOR FILING DATE: 2002-02-06  
; NUMBER OF SEQ ID NOS: 104  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 100  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:/No. US20030228371A1e  
=  
; OTHER INFORMATION: Synthetic Construct  
US-10-359-363A-100

Query Match 36.4%; Score 4; DB 15; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEGG 4  
|  
Db 5 AEGG 8

RESULT 28

US-09-828-592-10  
; Sequence 10, Application US/09828592  
; Patent No. US20010055591A1  
; GENERAL INFORMATION:  
; APPLICANT: Walston, Timothy  
; APPLICANT: Cooper, Scott  
; APPLICANT: Revzaie, Alireza  
; TITLE OF INVENTION: ANTITHROMBIN H-HELIX MUTANTS  
; FILE REFERENCE: 7869.10USU1  
; CURRENT APPLICATION NUMBER: US/09/828,592  
; CURRENT FILING DATE: 2001-04-06  
; PRIOR APPLICATION NUMBER: 60/195,872  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 10  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-828-592-10

Query Match 27.3%; Score 3; DB 9; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KKM 9  
|  
Db 9 KKM 11

RESULT 29

US-09-765-527-206  
; Sequence 206, Application US/09765527

```

; Patent No. US20020006638A1
;   GENERAL INFORMATION:
;       APPLICANT: Better, Marc D.
;       TITLE OF INVENTION: Methods for Recombinant Microbial Production of
;                               Fusion Proteins and BPI-Derived Peptides
;       NUMBER OF SEQUENCES: 265
;       CORRESPONDENCE ADDRESS:
;           ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
;           STREET: 6300 Sears Tower, 233 South Wacker Drive
;           CITY: Chicago
;           STATE: Illinois
;           COUNTRY: United States of America
;           ZIP: 60606-6402
;       COMPUTER READABLE FORM:
;           MEDIUM TYPE: Floppy disk
;           COMPUTER: IBM PC compatible
;           OPERATING SYSTEM: PC-DOS/MS-DOS
;           SOFTWARE: PatentIn Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;           APPLICATION NUMBER: US/09/765,527
;           FILING DATE: 18-Jan-2001
;       PRIOR APPLICATION DATA:
;           APPLICATION NUMBER: 08/621,803
;           FILING DATE: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;           NAME: Borun, Michael F.
;           REGISTRATION NUMBER: 25,447
;           REFERENCE/DOCKET NUMBER: 27129/33199
;       TELECOMMUNICATION INFORMATION:
;           TELEPHONE: 312/474-6300
;           TELEFAX: 312/474-0448
;           TELEX: 25-3856
;       INFORMATION FOR SEQ ID NO: 206:
;           SEQUENCE CHARACTERISTICS:
;               LENGTH: 11 amino acids
;               TYPE: amino acid
;               TOPOLOGY: linear
;           MOLECULE TYPE: peptide
;           FEATURE:
;               NAME/KEY: misc_feature
;               OTHER INFORMATION: "XMP.350"
;           FEATURE:
;               NAME/KEY: Modified-site
;               LOCATION: C-Terminus
;               OTHER INFORMATION: /label= Amidation
;                               /note= "The C-Terminus is Amidated."
;       SEQUENCE DESCRIPTION: SEQ ID NO: 206:
US-09-765-527-206

```

```

Query Match          27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      5 KKK 7
        |||
Db      1 KKK 3

```

RESULT 30

US-09-010-714-5

; Sequence 5, Application US/09010714  
 ; Patent No. US20020012942A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: McCarthy, James B.  
 ; APPLICANT: Furcht, Leo T.  
 ; APPLICANT: Iida, Joji  
 ; TITLE OF INVENTION: POLYPEPTIDES WITH ALPHA 4 INTEGRIN SUBUNIT RELATED  
 ; TITLE OF INVENTION: ACTIVITY  
 ; FILE REFERENCE: 600.332US01  
 ; CURRENT APPLICATION NUMBER: US/09/010,714  
 ; CURRENT FILING DATE: 1998-01-22  
 ; NUMBER OF SEQ ID NOS: 11  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 5  
 ; LENGTH: 11  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-010-714-5

Query Match 27.3%; Score 3; DB 9; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GKK 6  
 |||  
 Db 6 GKK 8

RESULT 31

US-09-811-672-24

; Sequence 24, Application US/09811672  
 ; Patent No. US20020052490A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: BALL, Tanja  
 ; APPLICANT: VRTALA, Susanne  
 ; APPLICANT: SPERR, Wolfgang  
 ; APPLICANT: VALENT, Peter  
 ; APPLICANT: SUSANI, Markus  
 ; APPLICANT: KRAFT, Dietrich  
 ; APPLICANT: VALENTA, Rudolf  
 ; APPLICANT: LAFFER, Sylvia  
 ; TITLE OF INVENTION: RECOMBINANT ALLERGEN, FRAGMENTS THEREOF, CORRESPONDING  
 RECOMBINANT DNA  
 ; TITLE OF INVENTION: MOLECULES, VECTORS AND HOSTS CONTAINING THE DNA  
 MOLECULES, DIAGNOSTIC AND  
 ; TITLE OF INVENTION: THERAPEUTIC USES OF SAID ALLERGENS AND FRAGMENTS  
 ; FILE REFERENCE: 1614-0247P  
 ; CURRENT APPLICATION NUMBER: US/09/811,672  
 ; CURRENT FILING DATE: 2001-03-20  
 ; NUMBER OF SEQ ID NOS: 28  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 24  
 ; LENGTH: 11  
 ; TYPE: PRT

; ORGANISM: Timothy Grass  
US-09-811-672-24

Query Match 27.3%; Score 3; DB 9; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EGG 4  
|||  
Db 5 EGG 7

RESULT 32

US-09-845-667-1

; Sequence 1, Application US/09845667

; Patent No. US20020065221A1

; GENERAL INFORMATION:

; APPLICANT: Cohen, Philip

; Alessi, Dario

; Cross, Darren

; TITLE OF INVENTION: CONTROL OF PROTEIN SYNTHESIS, AND SCREENING METHOD  
; FOR AGENTS

; NUMBER OF SEQUENCES: 58

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Braman & Rogalskyj, LLP

; STREET: P.O. Box 352

; CITY: Canandaigua

; STATE: New York

; COUNTRY: USA

; ZIP: 14424-0352

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/845,667

; FILING DATE: 30-Apr-2001

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 09/091,763

; FILING DATE: 19-JUN-1998

; APPLICATION NUMBER: PCT/GB96/03186

; FILING DATE: 20-DEC-1996

; APPLICATION NUMBER: GB 9526083.2

; FILING DATE: 20-DEC-1995

; APPLICATION NUMBER: GB 9610272.8

; FILING DATE: 16-MAY-1996

; APPLICATION NUMBER: GB 9615066.9

; FILING DATE: 18-JUL-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Braman, Susan J

; REGISTRATION NUMBER: 34,103

; REFERENCE/DOCKET NUMBER: 002.00041

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 716-393-3002

; TELEFAX: 716-393-3001

; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-09-845-667-1

Query Match 27.3%; Score 3; DB 9; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEG 3  
|||  
Db 9 AEG 11

RESULT 33  
US-09-873-676-6  
; Sequence 6, Application US/09873676  
; Patent No. US20020077289A1  
; GENERAL INFORMATION:  
; APPLICANT: MacDonald, Nicholas J.  
; APPLICANT: Sim, Kim L.  
; TITLE OF INVENTION: Angiostatin and Endostatin Binding Proteins and Methods  
of Use  
; FILE REFERENCE: 05213-0378 (43170-259333)  
; CURRENT APPLICATION NUMBER: US/09/873,676  
; CURRENT FILING DATE: 2001-06-04  
; PRIOR APPLICATION NUMBER: US 60/209,065  
; PRIOR FILING DATE: 2000-06-02  
; PRIOR APPLICATION NUMBER: US 60/289,387  
; PRIOR FILING DATE: 2001-05-08  
; NUMBER OF SEQ ID NOS: 123  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 6  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic binding peptide  
US-09-873-676-6

Query Match 27.3%; Score 3; DB 9; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EGG 4  
|||  
Db 7 EGG 9

RESULT 34  
US-09-873-676-19  
; Sequence 19, Application US/09873676

```

; Patent No. US20020077289A1
; GENERAL INFORMATION:
; APPLICANT: MacDonald, Nicholas J.
; APPLICANT: Sim, Kim L.
; TITLE OF INVENTION: Angiostatin and Endostatin Binding Proteins and Methods
of Use
; FILE REFERENCE: 05213-0378 (43170-259333)
; CURRENT APPLICATION NUMBER: US/09/873,676
; CURRENT FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: US 60/209,065
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: US 60/289,387
; PRIOR FILING DATE: 2001-05-08
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic binding peptide
US-09-873-676-19

```

```

Query Match          27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      2 EGG 4
      |||
Db      7 EGG 9

```

# RESULT 35

```

US-09-881-490-181
; Sequence 181, Application US/09881490
; Patent No. US20020077298A1
; GENERAL INFORMATION:
; APPLICANT: Little II, Roger G.
; Lim, Edward
; Fadem, Mitchell B.
; TITLE OF INVENTION: Anti-Fungal Peptides
; NUMBER OF SEQUENCES: 211
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th FloorDrive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/881,490
; FILING DATE: 14-Jun-2001

```

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/119,858
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/372,105
; FILING DATE: 13-JAN-95
; APPLICATION NUMBER: 08/306,473
; FILING DATE: 15-SEP-94
; APPLICATION NUMBER: 08/273,540
; FILING DATE: 11-JUL-94
; APPLICATION NUMBER: 08/209,762
; FILING DATE: 11-MAR-94
; APPLICATION NUMBER: 08/183,222
; FILING DATE: 14-JAN-94
; APPLICATION NUMBER: 08/093,202
; FILING DATE: 15-JUL-93
; APPLICATION NUMBER: 08/030,644
; FILING DATE: 12-MAR-93
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 100-238/11021US01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 181:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: "XMP.350"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: C-Terminus
; OTHER INFORMATION: /label= Amidation
; /note= "The C-Terminus is Amidated"
; SEQUENCE DESCRIPTION: SEQ ID NO: 181:
US-09-881-490-181

```

```

Query Match          27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      5 KKK 7
      |||
Db      1 KKK 3

```

```

RESULT 36
US-09-977-831-32
; Sequence 32, Application US/09977831
; Patent No. US20020120100A1
; GENERAL INFORMATION:
; APPLICANT: PACTT, Tech Transfer Office University of Lausanne

```



```
; APPLICANT: Bonny, Christophe
; TITLE OF INVENTION: INTRACELLULAR DELIVERY OF BIOLOGICAL EFFECTORS
; FILE REFERENCE: 20349-512 Transporter peptides
; CURRENT APPLICATION NUMBER: US/09/977,831
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/240,315
; PRIOR FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 32
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: TRANSPORTER
; OTHER INFORMATION: PEPTIDE
US-09-977-831-32
```

```
Query Match          27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;
```

```
Qy      3 G GK 5
      |||
Db      2 G GK 4
```

#### RESULT 37

US-09-966-871-37

```
; Sequence 37, Application US/09966871
; Patent No. US20020127539A1
; GENERAL INFORMATION:
; APPLICANT: Kopin, Alan S.
; TITLE OF INVENTION: Assays for Identifying Receptors Having
; TITLE OF INVENTION: Alterations in Signaling
; FILE REFERENCE: 00398/512002
; CURRENT APPLICATION NUMBER: US/09/966,871
; CURRENT FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US 60/236,302
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/288,644
; PRIOR FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-966-871-37
```

```
Query Match          27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;
```

```
Qy      4 G KK 6
      |||
Db      7 G KK 9
```

RESULT 38

US-09-739-068-23

; Sequence 23, Application US/09739068

; Patent No. US20020142297A1

; GENERAL INFORMATION:

; APPLICANT: Bogdanov, Alexei A.

; Weissleder, Ralph

; Simonova, Maria

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IMAGING  
; GENE EXPRESSION

; NUMBER OF SEQUENCES: 24

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson P.C.

; STREET: 225 Franklin Street

; CITY: Boston

; STATE: MA

; COUNTRY: US

; ZIP: 02110-2804

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: Windows95

; SOFTWARE: FastSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/739,068

; FILING DATE: 18-Dec-2000

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/09/015,366B

; FILING DATE: 29-JAN-1998

; APPLICATION NUMBER: 60/037,350

; FILING DATE: 31-JAN-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Fasse, Peter J.

; REGISTRATION NUMBER: 32,983

; REFERENCE/DOCKET NUMBER: 00786/388002

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617/542-5070

; TELEFAX: 617/542-8906

; TELEX: 200154

; INFORMATION FOR SEQ ID NO: 23:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; SEQUENCE DESCRIPTION: SEQ ID NO: 23:

US-09-739-068-23

Query Match 27.3%; Score 3; DB 9; Length 11;

Best Local Similarity 100.0%; Pred. No. 1.1e+04;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EGG 4

|||

Db 2 EGG 4

RESULT 39

US-09-823-829-36

; Sequence 36, Application US/09823829  
 ; Patent No. US20020146697A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Yamamoto, Satoshi  
 ; APPLICANT: Nakamura, Shoko  
 ; APPLICANT: Suzuki, Makoto  
 ; APPLICANT: Kasai, Hiroaki  
 ; APPLICANT: Hamada, Tohru  
 ; TITLE OF INVENTION: METHOD FOR IDENTIFICATION AND DETECTION OF MICROORGANISMS  
 ; TITLE OF INVENTION: USING GYRASE GENE AS AN INDICATOR  
 ; FILE REFERENCE: 12817-004001  
 ; CURRENT APPLICATION NUMBER: US/09/823,829  
 ; CURRENT FILING DATE: 2001-03-30  
 ; PRIOR APPLICATION NUMBER: US 09/208,688  
 ; PRIOR FILING DATE: 1998-12-10  
 ; PRIOR APPLICATION NUMBER: JP 97/343316  
 ; PRIOR FILING DATE: 1997-12-12  
 ; NUMBER OF SEQ ID NOS: 82  
 ; SOFTWARE: PatentIn version 2.0  
 ; SEQ ID NO 36  
 ; LENGTH: 11  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: synthetically generated peptide  
 US-09-823-829-36

Query Match 27.3%; Score 3; DB 9; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EGG 4  
 |||  
 Db 7 EGG 9

RESULT 40

US-09-823-829-37

; Sequence 37, Application US/09823829  
 ; Patent No. US20020146697A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Yamamoto, Satoshi  
 ; APPLICANT: Nakamura, Shoko  
 ; APPLICANT: Suzuki, Makoto  
 ; APPLICANT: Kasai, Hiroaki  
 ; APPLICANT: Hamada, Tohru  
 ; TITLE OF INVENTION: METHOD FOR IDENTIFICATION AND DETECTION OF MICROORGANISMS  
 ; TITLE OF INVENTION: USING GYRASE GENE AS AN INDICATOR  
 ; FILE REFERENCE: 12817-004001  
 ; CURRENT APPLICATION NUMBER: US/09/823,829  
 ; CURRENT FILING DATE: 2001-03-30  
 ; PRIOR APPLICATION NUMBER: US 09/208,688  
 ; PRIOR FILING DATE: 1998-12-10

; PRIOR APPLICATION NUMBER: JP 97/343316  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 82  
; SOFTWARE: PatentIn version 2.0  
; SEQ ID NO 37  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetically generated peptide  
US-09-823-829-37

Query Match 27.3%; Score 3; DB 9; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EGG 4  
|||  
Db 7 EGG 9

RESULT 41

US-09-781-988-17

; Sequence 17, Application US/09781988  
; Patent No. US20020150881A1  
; GENERAL INFORMATION:  
; APPLICANT: Ladner, Robert Charles  
; Guterman, Sonia Kosow  
; Roberts, Bruce Lindsay  
; Markland, William  
; Ley, Arthur Charles  
; Kent, Rachel Baribault  
; TITLE OF INVENTION: Directed Evolution of No. US20020150881A1e1  
; Binding Proteins  
; NUMBER OF SEQUENCES: 121  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Browdy and Neimark  
; STREET: 419 Seventh Street, N.W.  
; Suite 300  
; CITY: Washington,  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WORDPERFECT 4.2  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/781,988  
; FILING DATE: 14-Feb-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/664,989  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: 07/487,063  
; FILING DATE: 02-MAR-1990

; APPLICATION NUMBER: 07/240,160  
 ; FILING DATE: 02-SEP-1988  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Cooper, Iver P.  
 ; REGISTRATION NUMBER: 28005  
 ; REFERENCE/DOCKET NUMBER: LADNER 7  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 202-628-5197  
 ; TELEFAX: 202-737-3528  
 ; INFORMATION FOR SEQ ID NO: 17:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 11 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 17:  
 US-09-781-988-17

Query Match 27.3%; Score 3; DB 9; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEG 3  
 |||  
 Db 9 AEG 11

#### RESULT 42

US-09-969-192-19

; Sequence 19, Application US/09969192  
 ; Patent No. US20020151027A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: WICKHAM, THOMAS J.  
 ; ROELVINK, PETRUS W.  
 ; KOVESDI, IMRE  
 ; TITLE OF INVENTION: TARGETING ADENOVIRUS WITH USE OF  
 ; CONSTRAINED PEPTIDE MOTIFS  
 ; NUMBER OF SEQUENCES: 80  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Leydig, Voit & Mayer, Ltd.  
 ; STREET: Two Prudential Plaza - 49th Floor  
 ; CITY: Chicago  
 ; STATE: Illinois  
 ; COUNTRY: USA  
 ; ZIP: 60601  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/969,192  
 ; FILING DATE: 01-Oct-2001  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 9-455061  
 ; FILING DATE: 06-DEC-1999  
 ; APPLICATION NUMBER: US 9-130225

```

;          FILING DATE: 06-AUG-1998
;          APPLICATION NUMBER: US 8-701124
;          FILING DATE: 21-AUG-1996
;          ATTORNEY/AGENT INFORMATION:
;          NAME: Hefner, M. Daniel
;          REGISTRATION NUMBER: 41,826
;          REFERENCE/DOCKET NUMBER: 213564
;          INFORMATION FOR SEQ ID NO: 19:
;          SEQUENCE CHARACTERISTICS:
;          LENGTH: 11 amino acids
;          TYPE: amino acid
;          TOPOLOGY: linear
;          MOLECULE TYPE: peptide
;          SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-969-192-19

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Query Match          27.3%;  Score 3;  DB 9;  Length 11;
Best Local Similarity 100.0%;  Pred. No. 1.1e+04;
Matches      3;  Conservative    0;  Mismatches    0;  Indels      0;  Gaps      0;

```

```

Qy          5 KKK 7
            |||
Db          3 KKK 5

```

RESULT 43

US-09-071-838-253

; Sequence 253, Application US/09071838

; Patent No. US20020152501A1

; GENERAL INFORMATION:

; APPLICANT: Fischer, Robert L.

; APPLICANT: Ohad, Nir

; APPLICANT: Kiyosue, Tomohiro

; APPLICANT: Yadegari, Ramin

; APPLICANT: Margossian, Linda

; APPLICANT: Harada, John

; APPLICANT: Goldberg, Robert B.

; TITLE OF INVENTION: Nucleic Acids That Control Seed and

; TITLE OF INVENTION: Fruit Development in Plants

; NUMBER OF SEQUENCES: 324

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP

; STREET: Two Embarcadero Center, Eighth Floor

; CITY: San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94111-3834

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/071,838

; FILING DATE: 01-MAY-1998

; CLASSIFICATION: 800

; ATTORNEY/AGENT INFORMATION:

; NAME: Bastian, Kevin L.  
; REGISTRATION NUMBER: 34,774  
; REFERENCE/DOCKET NUMBER: 023070-086100US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 253:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-09-071-838-253

Query Match 27.3%; Score 3; DB 9; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KMR 10  
|||  
Db 7 KMR 9

RESULT 44

US-09-823-823-36

; Sequence 36, Application US/09823823

; Patent No. US20020171092A1

; GENERAL INFORMATION:

; APPLICANT: Yamamoto, Satoshi

; APPLICANT: Kasai, Hiroaki

; APPLICANT: Nakamura, Shoko

; APPLICANT: Suzuki, Makoto

; APPLICANT: Hamoda, Tohru

; TITLE OF INVENTION: METHOD FOR IDENTIFICATION AND DETECTION OF MICROORGANISMS  
USING GYRASE

; TITLE OF INVENTION: GENE AS AN INDICATOR

; FILE REFERENCE: 12817-004001

; CURRENT APPLICATION NUMBER: US/09/823,823

; CURRENT FILING DATE: 2001-03-30

; PRIOR APPLICATION NUMBER: US 09/208,688

; PRIOR FILING DATE: 1998-12-10

; PRIOR APPLICATION NUMBER: JP 97/343316

; PRIOR FILING DATE: 1997-12-12

; NUMBER OF SEQ ID NOS: 80

; SOFTWARE: PatentIn version 2.0

; SEQ ID NO 36

; LENGTH: 11

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Synthetically generated protein

US-09-823-823-36

Query Match 27.3%; Score 3; DB 9; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EGG 4  
|||  
Db 7 EGG 9

RESULT 45

US-09-823-823-37

; Sequence 37, Application US/09823823

; Patent No. US20020171092A1

; GENERAL INFORMATION:

; APPLICANT: Yamamoto, Satoshi

; APPLICANT: Kasai, Hiroaki

; APPLICANT: Nakamura, Shoko

; APPLICANT: Suzuki, Makoto

; APPLICANT: Hamoda, Tohru

; TITLE OF INVENTION: METHOD FOR IDENTIFICATION AND DETECTION OF MICROORGANISMS  
USING GYRASE

; TITLE OF INVENTION: GENE AS AN INDICATOR

; FILE REFERENCE: 12817-004001

; CURRENT APPLICATION NUMBER: US/09/823,823

; CURRENT FILING DATE: 2001-03-30

; PRIOR APPLICATION NUMBER: US 09/208,688

; PRIOR FILING DATE: 1998-12-10

; PRIOR APPLICATION NUMBER: JP 97/343316

; PRIOR FILING DATE: 1997-12-12

; NUMBER OF SEQ ID NOS: 80

; SOFTWARE: PatentIn version 2.0

; SEQ ID NO 37

; LENGTH: 11

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Synthetically generated protein

US-09-823-823-37

Query Match 27.3%; Score 3; DB 9; Length 11;

Best Local Similarity 100.0%; Pred. No. 1.1e+04;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EGG 4  
|||  
Db 7 EGG 9

RESULT 46

US-09-965-967-26

; Sequence 26, Application US/09965967

; Patent No. US20020177557A1

; GENERAL INFORMATION:

; APPLICANT: Shi, Yigong

; TITLE OF INVENTION: Compositions And Methods For Regulating Apoptosis

; FILE REFERENCE: PU-0031 (01-1739-1)

; CURRENT APPLICATION NUMBER: US/09/965,967

; CURRENT FILING DATE: 2001-09-28

; PRIOR APPLICATION NUMBER: 60/236,574

; PRIOR FILING DATE: 2000-09-29

; PRIOR APPLICATION NUMBER: 60/256,830



; PRIOR FILING DATE: 2000-12-20  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 26  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Drosophila melanogaster  
US-09-965-967-26

Query Match 27.3%; Score 3; DB 9; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EGG 4  
|||  
Db 9 EGG 11

RESULT 47

US-09-999-724-76  
; Sequence 76, Application US/09999724  
; Publication No. US20030022355A1  
; GENERAL INFORMATION:  
; APPLICANT: WICKHAM, THOMAS J.  
; APPLICANT: KOVESDI, IMRE  
; APPLICANT: BROUGH, DOUGLAS E.  
; TITLE OF INVENTION: VECTORS AND METHODS FOR GENE TRANSFER  
; FILE REFERENCE: 212960  
; CURRENT APPLICATION NUMBER: US/09/999,724  
; CURRENT FILING DATE: 2001-10-24  
; PRIOR APPLICATION NUMBER: US 09/101,751  
; PRIOR FILING DATE: 1999-01-29  
; PRIOR APPLICATION NUMBER: WO 96US19150  
; PRIOR FILING DATE: 1996-11-27  
; PRIOR APPLICATION NUMBER: US 08/700,846  
; PRIOR FILING DATE: 1996-08-21  
; PRIOR APPLICATION NUMBER: US 08/701,124  
; PRIOR FILING DATE: 1996-08-21  
; PRIOR APPLICATION NUMBER: US 08/563,368  
; PRIOR FILING DATE: 1995-11-28  
; NUMBER OF SEQ ID NOS: 94  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 76  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-09-999-724-76

Query Match 27.3%; Score 3; DB 10; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KKK 7  
|||  
Db 3 KKK 5

RESULT 48

US-09-931-325A-131

; Sequence 131, Application US/09931325A  
 ; Publication No. US20030054337A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Birkett, Ashley J.  
 ; TITLE OF INVENTION: MALARIA IMMUNOGEN AND VACCINE  
 ; FILE REFERENCE: 4564/83503 ICC-103.1  
 ; CURRENT APPLICATION NUMBER: US/09/931,325A  
 ; CURRENT FILING DATE: 2002-02-22  
 ; PRIOR APPLICATION NUMBER: 60/225,843  
 ; PRIOR FILING DATE: 2000-08-16  
 ; PRIOR APPLICATION NUMBER: USSN NOT YET ASSIGND  
 ; PRIOR FILING DATE: 2001-08-15  
 ; NUMBER OF SEQ ID NOS: 186  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 131

; LENGTH: 11  
 ; TYPE: PRT  
 ; ORGANISM: Human immunodeficiency virus type 1  
 US-09-931-325A-131

Query Match 27.3%; Score 3; DB 10; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GGK 5  
 |||  
 Db 9 GGK 11

RESULT 49

US-09-931-325A-158

; Sequence 158, Application US/09931325A  
 ; Publication No. US20030054337A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Birkett, Ashley J.  
 ; TITLE OF INVENTION: MALARIA IMMUNOGEN AND VACCINE  
 ; FILE REFERENCE: 4564/83503 ICC-103.1  
 ; CURRENT APPLICATION NUMBER: US/09/931,325A  
 ; CURRENT FILING DATE: 2002-02-22  
 ; PRIOR APPLICATION NUMBER: 60/225,843  
 ; PRIOR FILING DATE: 2000-08-16  
 ; PRIOR APPLICATION NUMBER: USSN NOT YET ASSIGND  
 ; PRIOR FILING DATE: 2001-08-15  
 ; NUMBER OF SEQ ID NOS: 186  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 158

; LENGTH: 11  
 ; TYPE: PRT  
 ; ORGANISM: Plasmodium vivax  
 US-09-931-325A-158

Query Match 27.3%; Score 3; DB 10; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EGG 4  
|||  
Db 7 EGG 9

RESULT 50

US-09-876-904A-25

; Sequence 25, Application US/09876904A

; Publication No. US20030072794A1

; GENERAL INFORMATION:

; APPLICANT: BOULIKAS, TENI

; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC

; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE

; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES

; FILE REFERENCE: TB-2002.00

; CURRENT APPLICATION NUMBER: US/09/876,904A

; CURRENT FILING DATE: 2001-06-08

; PRIOR APPLICATION NUMBER: US 60/210,925

; PRIOR FILING DATE: 2000-06-09

; NUMBER OF SEQ ID NOS: 629

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 25

; LENGTH: 11

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic SV40 large T

; OTHER INFORMATION: protein

US-09-876-904A-25

Query Match 27.3%; Score 3; DB 10; Length 11;

Best Local Similarity 100.0%; Pred. No. 1.1e+04;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KKK 7  
|||  
Db 5 KKK 7

RESULT 51

US-09-876-904A-77

; Sequence 77, Application US/09876904A

; Publication No. US20030072794A1

; GENERAL INFORMATION:

; APPLICANT: BOULIKAS, TENI

; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC

; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE

; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES

; FILE REFERENCE: TB-2002.00

; CURRENT APPLICATION NUMBER: US/09/876,904A

; CURRENT FILING DATE: 2001-06-08  
; PRIOR APPLICATION NUMBER: US 60/210,925  
; PRIOR FILING DATE: 2000-06-09  
; NUMBER OF SEQ ID NOS: 629  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 77  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide crosslinked  
; OTHER INFORMATION: to bovine serum albumin  
US-09-876-904A-77

Query Match 27.3%; Score 3; DB 10; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KKK 7  
|||  
Db 6 KKK 8

RESULT 52

US-09-876-904A-273  
; Sequence 273, Application US/09876904A  
; Publication No. US20030072794A1  
; GENERAL INFORMATION:  
; APPLICANT: BOULIKAS, TENI  
; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC  
; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE  
; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES  
; FILE REFERENCE: TB-2002.00  
; CURRENT APPLICATION NUMBER: US/09/876,904A  
; CURRENT FILING DATE: 2001-06-08  
; PRIOR APPLICATION NUMBER: US 60/210,925  
; PRIOR FILING DATE: 2000-06-09  
; NUMBER OF SEQ ID NOS: 629  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 273  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Drosophila sp.  
; FEATURE:  
; OTHER INFORMATION: Recombination repair protein 1  
US-09-876-904A-273

Query Match 27.3%; Score 3; DB 10; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KKK 7  
|||  
Db 6 KKK 8

RESULT 53

US-09-876-904A-354

; Sequence 354, Application US/09876904A  
 ; Publication No. US20030072794A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: BOULIKAS, TENI  
 ; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC  
 ; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE  
 ; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES  
 ; FILE REFERENCE: TB-2002.00  
 ; CURRENT APPLICATION NUMBER: US/09/876,904A  
 ; CURRENT FILING DATE: 2001-06-08  
 ; PRIOR APPLICATION NUMBER: US 60/210,925  
 ; PRIOR FILING DATE: 2000-06-09  
 ; NUMBER OF SEQ ID NOS: 629  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 354  
 ; LENGTH: 11  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; OTHER INFORMATION: Human ATF-3 (in basic region that binds DNA)  
 US-09-876-904A-354

Query Match 27.3%; Score 3; DB 10; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KKK 7  
 |||  
 Db 6 KKK 8

RESULT 54

US-09-876-904A-373

; Sequence 373, Application US/09876904A  
 ; Publication No. US20030072794A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: BOULIKAS, TENI  
 ; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC  
 ; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE  
 ; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES  
 ; FILE REFERENCE: TB-2002.00  
 ; CURRENT APPLICATION NUMBER: US/09/876,904A  
 ; CURRENT FILING DATE: 2001-06-08  
 ; PRIOR APPLICATION NUMBER: US 60/210,925  
 ; PRIOR FILING DATE: 2000-06-09  
 ; NUMBER OF SEQ ID NOS: 629  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 373  
 ; LENGTH: 11

; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: MBP-1 (class I MHC enhancer binding protein  
; OTHER INFORMATION: 1) mw 200 kD.  
US-09-876-904A-373

Query Match 27.3%; Score 3; DB 10; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KKK 7  
|||  
Db 3 KKK 5

RESULT 55

US-09-876-904A-544  
; Sequence 544, Application US/09876904A  
; Publication No. US20030072794A1  
; GENERAL INFORMATION:  
; APPLICANT: BOULIKAS, TENI  
; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND  
THERAPEUTIC  
; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC  
PEPTIDE  
; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES  
; FILE REFERENCE: TB-2002.00  
; CURRENT APPLICATION NUMBER: US/09/876,904A  
; CURRENT FILING DATE: 2001-06-08  
; PRIOR APPLICATION NUMBER: US 60/210,925  
; PRIOR FILING DATE: 2000-06-09  
; NUMBER OF SEQ ID NOS: 629  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 544  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Rattus sp.  
; FEATURE:  
; OTHER INFORMATION: Rat L17 ribosomal protein (184 aas).  
US-09-876-904A-544

Query Match 27.3%; Score 3; DB 10; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KKK 7  
|||  
Db 1 KKK 3

RESULT 56

US-09-876-904A-597  
; Sequence 597, Application US/09876904A  
; Publication No. US20030072794A1  
; GENERAL INFORMATION:  
; APPLICANT: BOULIKAS, TENI

```
; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND
THERAPEUTIC
; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC
PEPTIDE
; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
; FILE REFERENCE: TB-2002.00
; CURRENT APPLICATION NUMBER: US/09/876,904A
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,925
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 629
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 597
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Parechinus angulosus
; FEATURE:
; OTHER INFORMATION: Sea urchin Parechinus angulosus sperm H1 (248 aa).
US-09-876-904A-597
```

```
Query Match          27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;
```

```
Qy          5 KKK 7
             |||
Db          8 KKK 10
```

```
RESULT 57
US-09-852-910-238
; Sequence 238, Application US/09852910
; Publication No. US20030096297A1
; GENERAL INFORMATION:
; APPLICANT: Hamm, Heidi
; APPLICANT: Gilchrist, Annette
; TITLE OF INVENTION: Method For Identifying Inhibitors of G Protein Coupled
Receptor Signaling
; FILE REFERENCE: 2661-101
; CURRENT APPLICATION NUMBER: US/09/852,910
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US 60/275,472
; PRIOR FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 271
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 238
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(11)
; OTHER INFORMATION: G13 library peptide
US-09-852-910-238
```

```
Query Match          27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
```

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 MRA 11  
|||  
Db 1 MRA 3

RESULT 58

US-09-972-656-7

; Sequence 7, Application US/09972656

; Publication No. US20030099647A1

; GENERAL INFORMATION:

; APPLICANT: Deshpande, Rajendra

; APPLICANT: Tsai, Mei-Mei

; TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma

; TITLE OF INVENTION: Neutralizing Activity

; FILE REFERENCE: A-799

; CURRENT APPLICATION NUMBER: US/09/972,656

; CURRENT FILING DATE: 2001-10-05

; NUMBER OF SEQ ID NOS: 135

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 7

; LENGTH: 11

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-972-656-7

Query Match 27.3%; Score 3; DB 10; Length 11;

Best Local Similarity 100.0%; Pred. No. 1.1e+04;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GSK 5  
|||  
Db 6 GSK 8

RESULT 59

US-09-893-878-17

; Sequence 17, Application US/09893878

; Publication No. US20030113717A1

; GENERAL INFORMATION:

; APPLICANT: Ladner, Robert Charles

; Guterman, Sonia Kosow

; Roberts, Bruce Lindsay

; Markland, William

; Ley, Arthur Charles

; Kent, Rachel Baribault

; TITLE OF INVENTION: Directed Evolution of No. US20030113717A1e1  
Binding Proteins

; NUMBER OF SEQUENCES: 121

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Browdy and Neimark

; STREET: 419 Seventh Street, N.W.

; Suite 300

; CITY: Washington,

; STATE: DC



```

;          COUNTRY: USA
;          ZIP: 20004
;    COMPUTER READABLE FORM:
;          MEDIUM TYPE: Floppy disk
;          COMPUTER: IBM PC compatible
;          OPERATING SYSTEM: PC-DOS/MS-DOS
;          SOFTWARE: WORDPERFECT 5.1
;    CURRENT APPLICATION DATA:
;          APPLICATION NUMBER: US/09/893,878
;          FILING DATE: 29-Jun-2001
;          CLASSIFICATION: <Unknown>
;    PRIOR APPLICATION DATA:
;          APPLICATION NUMBER: 08/009,319
;          FILING DATE: <Unknown>
;          APPLICATION NUMBER: 07/664,989
;          FILING DATE: 01-MAR-1991
;          APPLICATION NUMBER: PCT/US89/03731
;          FILING DATE: 01-SEP-1989
;          APPLICATION NUMBER: 07/487,063
;          FILING DATE: 02-MAR-1990
;          APPLICATION NUMBER: 07/240,160
;          FILING DATE: 02-SEP-1988
;    ATTORNEY/AGENT INFORMATION:
;          NAME: Cooper, Iver P.
;          REGISTRATION NUMBER: 28005
;          REFERENCE/DOCKET NUMBER: LADNER 7
;    TELECOMMUNICATION INFORMATION:
;          TELEPHONE: 202-628-5197
;          TELEFAX: 202-737-3528
;    INFORMATION FOR SEQ ID NO: 17:
;          SEQUENCE CHARACTERISTICS:
;            LENGTH: 11 amino acids
;            TYPE: amino acid
;            TOPOLOGY: linear
;          MOLECULE TYPE: protein
;          SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-893-878-17

```

```

Query Match          27.3%;  Score 3;  DB 10;  Length 11;
Best Local Similarity 100.0%;  Pred. No. 1.1e+04;
Matches      3;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

```

```

Qy          1 AEG 3
            |||
Db          9 AEG 11

```

```

RESULT 60
US-09-930-915A-172
; Sequence 172, Application US/09930915A
; Publication No. US20030138769A1
; GENERAL INFORMATION:
; APPLICANT: Birkett, Ashley J.
; TITLE OF INVENTION: IMMUNOGENIC HBc CHIMER PARTICLES HAVING ENHANCED
; TITLE OF INVENTION: STABILITY
; FILE REFERENCE: 4564/83501 ICC-102.2 PCT
; CURRENT APPLICATION NUMBER: US/09/930,915A

```

; CURRENT FILING DATE: 2001-08-15  
; PRIOR APPLICATION NUMBER: 60/226,867  
; PRIOR FILING DATE: 2000-08-22  
; PRIOR APPLICATION NUMBER: 60/225,843  
; PRIOR FILING DATE: 2000-08-16  
; NUMBER OF SEQ ID NOS: 313  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 172  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Human immunodeficiency virus type 1  
US-09-930-915A-172

Query Match 27.3%; Score 3; DB 10; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GGK 5  
|||  
Db 9 GGK 11

RESULT 61

US-09-930-915A-195  
; Sequence 195, Application US/09930915A  
; Publication No. US20030138769A1  
; GENERAL INFORMATION:  
; APPLICANT: Birkett, Ashley J.  
; TITLE OF INVENTION: IMMUNOGENIC HBc CHIMER PARTICLES HAVING ENHANCED  
; TITLE OF INVENTION: STABILITY  
; FILE REFERENCE: 4564/83501 ICC-102.2 PCT  
; CURRENT APPLICATION NUMBER: US/09/930,915A  
; CURRENT FILING DATE: 2001-08-15  
; PRIOR APPLICATION NUMBER: 60/226,867  
; PRIOR FILING DATE: 2000-08-22  
; PRIOR APPLICATION NUMBER: 60/225,843  
; PRIOR FILING DATE: 2000-08-16  
; NUMBER OF SEQ ID NOS: 313  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 195  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Plasmodium vivax  
US-09-930-915A-195

Query Match 27.3%; Score 3; DB 10; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EGG 4  
|||  
Db 7 EGG 9

RESULT 62

US-09-933-767-1184  
; Sequence 1184, Application US/099333767

; Publication No. US20030181692A1  
; GENERAL INFORMATION:  
; APPLICANT: Ni et al.  
; TITLE OF INVENTION: 207 Human Secreted Proteins  
; FILE REFERENCE: PZ007P2  
; CURRENT APPLICATION NUMBER: US/09/933,767  
; CURRENT FILING DATE: 2001-08-22  
; PRIOR APPLICATION NUMBER: PCT/US01/05614  
; PRIOR FILING DATE: 2001-02-21  
; PRIOR APPLICATION NUMBER: 60/184,836  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: 60/193,170  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: 09/205,258  
; PRIOR FILING DATE: 1998-12-04  
; PRIOR APPLICATION NUMBER: PCT/US98/11422  
; PRIOR FILING DATE: 1998-06-04  
; PRIOR APPLICATION NUMBER: 60/048,885  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/049,375  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,881  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,880  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,896  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/049,020  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,876  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,895  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,884  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,894  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,971  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,964  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,882  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,899  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,893  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,900  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,901  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,892  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,915  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/049,019  
; PRIOR FILING DATE: 1997-06-06

; PRIOR APPLICATION NUMBER: 60/048,970  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,972  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,916  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/049,373  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,875  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/049,374  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,917  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,949  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,974  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,883  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,897  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,898  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,962  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,963  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,877  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,878  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/068,054  
; PRIOR FILING DATE: 1997-12-18  
; PRIOR APPLICATION NUMBER: 60/068,064  
; PRIOR FILING DATE: 1997-12-18  
; PRIOR APPLICATION NUMBER: 60/068,053  
; PRIOR FILING DATE: 1997-12-18  
; PRIOR APPLICATION NUMBER: 60/070,923  
; PRIOR FILING DATE: 1997-12-18  
; PRIOR APPLICATION NUMBER: 60/073,160  
; PRIOR FILING DATE: 1998-01-30  
; PRIOR APPLICATION NUMBER: 60/073,159  
; PRIOR FILING DATE: 1998-01-30  
; PRIOR APPLICATION NUMBER: 60/073,165  
; PRIOR FILING DATE: 1998-01-30  
; PRIOR APPLICATION NUMBER: 60/073,164  
; PRIOR FILING DATE: 1998-01-30  
; PRIOR APPLICATION NUMBER: 60/085,925  
; PRIOR FILING DATE: 1998-05-18  
; PRIOR APPLICATION NUMBER: 60/085,921  
; PRIOR FILING DATE: 1998-05-18  
; PRIOR APPLICATION NUMBER: 60/085,923  
; PRIOR FILING DATE: 1998-05-18  
; PRIOR APPLICATION NUMBER: 60/085,922  
; PRIOR FILING DATE: 1998-05-18  
; PRIOR APPLICATION NUMBER: 60/092,921

; PRIOR FILING DATE: 1998-07-15  
; PRIOR APPLICATION NUMBER: 60/094,657  
; PRIOR FILING DATE: 1998-07-30  
; NUMBER OF SEQ ID NOS: 1245  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1184  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-933-767-1184

Query Match 27.3%; Score 3; DB 10; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEG 3  
|||  
Db 8 AEG 10

RESULT 63

US-09-896-095-17  
; Sequence 17, Application US/09896095  
; Publication No. US20030219886A1  
; GENERAL INFORMATION:  
; APPLICANT: LADNER, Charles C.  
; APPLICANT: GUTERMAN, Sonia K.  
; APPLICANT: ROBERTS, Bruce L.  
; APPLICANT: MARKLAND, William  
; APPLICANT: LEY, Arthur C.  
; APPLICANT: KENT, Rachel B.  
; TITLE OF INVENTION: DIRECTED EVOLUTION OF NOVEL BINDING PROTEINS  
; FILE REFERENCE: LADNER=7L  
; CURRENT APPLICATION NUMBER: US/09/896,095  
; CURRENT FILING DATE: 2001-06-29  
; PRIOR APPLICATION NUMBER: 08/415,922  
; PRIOR FILING DATE: 1995-03-04  
; PRIOR APPLICATION NUMBER: 08/009,319  
; PRIOR FILING DATE: 1993-01-26  
; PRIOR APPLICATION NUMBER: 07/664,989  
; PRIOR FILING DATE: 1991-03-01  
; PRIOR APPLICATION NUMBER: 08/993,776  
; PRIOR FILING DATE: 1997-12-18  
; NUMBER OF SEQ ID NOS: 274  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 17  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: synthetic, EGGGS linker at NarI site of gene of Table 113  
US-09-896-095-17

Query Match 27.3%; Score 3; DB 11; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEG 3  
|||  
Db 9 AEG 11

RESULT 64

US-10-361-270-18

; Sequence 18, Application US/10361270  
; Publication No. US20040038299A1  
; GENERAL INFORMATION:  
; APPLICANT: Kuai, Jun  
; APPLICANT: Wooters, Joseph L  
; APPLICANT: Nickbarg, Elliott  
; APPLICANT: Qiu, Yongchang  
; APPLICANT: Lin, Lih-Ling  
; TITLE OF INVENTION: Composition and Method for Modulating an Inflammatory  
; TITLE OF INVENTION: Response  
; FILE REFERENCE: 22058-565  
; CURRENT APPLICATION NUMBER: US/10/361,270  
; CURRENT FILING DATE: 2003-02-10  
; PRIOR APPLICATION NUMBER: 60/355,183  
; PRIOR FILING DATE: 2002-02-08  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 18  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of  
; OTHER INFORMATION: TRAF2 protein.  
US-10-361-270-18

Query Match 27.3%; Score 3; DB 12; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GKK 6  
|||  
Db 9 GKK 11

RESULT 65

US-10-458-860-37

; Sequence 37, Application US/10458860  
; Publication No. US20040049800A1  
; GENERAL INFORMATION:  
; APPLICANT: Kopin, Alan S.  
; APPLICANT: Beinborn, Martin  
; TITLE OF INVENTION: Rapid Methods For Assessing Therapeutic  
; TITLE OF INVENTION: Activity Using Animals Expressing Constitutively Active  
G  
; TITLE OF INVENTION: Protein-Coupled Receptors  
; FILE REFERENCE: 00398/517002  
; CURRENT APPLICATION NUMBER: US/10/458,860  
; CURRENT FILING DATE: 2003-06-11  
; PRIOR APPLICATION NUMBER: US 60/388,450

; PRIOR FILING DATE: 2002-06-13  
; NUMBER OF SEQ ID NOS: 87  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 37  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic fragment  
US-10-458-860-37

Query Match 27.3%; Score 3; DB 12; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GKK 6  
|||  
Db 7 GKK 9

RESULT 66

US-10-653-595-458

; Sequence 458, Application US/10653595  
; Publication No. US20040048304A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et. al.  
; TITLE OF INVENTION: 95 Human secreted proteins  
; FILE REFERENCE: PZ027P1C1  
; CURRENT APPLICATION NUMBER: US/10/653,595  
; CURRENT FILING DATE: 2003-09-03  
; PRIOR APPLICATION NUMBER: US 09/397945  
; PRIOR FILING DATE: 1999-09-17  
; PRIOR APPLICATION NUMBER: PCT/US99/05804  
; PRIOR FILING DATE: 1999-03-18  
; PRIOR APPLICATION NUMBER: 60/078,566  
; PRIOR FILING DATE: 1998-03-19  
; PRIOR APPLICATION NUMBER: 60/078,576  
; PRIOR FILING DATE: 1998-03-19  
; PRIOR APPLICATION NUMBER: 60/078,573  
; PRIOR FILING DATE: 1998-03-19  
; PRIOR APPLICATION NUMBER: 60/078,574  
; PRIOR FILING DATE: 1998-03-19  
; PRIOR APPLICATION NUMBER: 60/078,579  
; PRIOR FILING DATE: 1998-03-19  
; PRIOR APPLICATION NUMBER: 60/080,314  
; PRIOR FILING DATE: 1998-04-01  
; PRIOR APPLICATION NUMBER: 60/080,312  
; PRIOR FILING DATE: 1998-04-01  
; PRIOR APPLICATION NUMBER: 60/078,578  
; PRIOR FILING DATE: 1998-03-19  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 470  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 458  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Homo sapiens

US-10-653-595-458

Query Match 27.3%; Score 3; DB 12; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KKK 7  
|||  
Db 7 KKK 9

RESULT 67

US-10-601-837-222

; Sequence 222, Application US/10601837  
; Publication No. US20040053309A1  
; GENERAL INFORMATION:  
; APPLICANT: Holt, Gordon D  
; APPLICANT: Kelly, Michael D  
; APPLICANT: Kennedy, Sandra J  
; APPLICANT: Moyses, Christopher  
; TITLE OF INVENTION: Proteins, Genes and Their Use for Diagnosis and Treatment  
of Kidney  
; TITLE OF INVENTION: Response  
; FILE REFERENCE: 2543-1-030  
; CURRENT APPLICATION NUMBER: US/10/601,837  
; CURRENT FILING DATE: 2003-06-23  
; PRIOR APPLICATION NUMBER: PCT/GB01/05777  
; PRIOR FILING DATE: 2001-12-24  
; PRIOR APPLICATION NUMBER: US 60/260392  
; PRIOR FILING DATE: 2000-12-29  
; NUMBER OF SEQ ID NOS: 272  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 222  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Ratus No. US20040053309Alvegicus  
US-10-601-837-222

Query Match 27.3%; Score 3; DB 12; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEG 3  
|||  
Db 5 AEG 7

RESULT 68

US-10-668-400-17

; Sequence 17, Application US/10668400  
; Publication No. US20040058859A1  
; GENERAL INFORMATION:  
; APPLICANT: Bay, Sylvie  
; APPLICANT: Cantacuzene, Daniele  
; APPLICANT: Leclerc, Claude  
; APPLICANT: Lo-Man, Richard  
; TITLE OF INVENTION: MULTIPLE ANTIGEN GLYCOPEPTIDE CARBOHYDRATE,



```
; TITLE OF INVENTION: VACCINE COMPRISING THE SAME AND USE THEREOF
; FILE REFERENCE: 102.166A-1
; CURRENT APPLICATION NUMBER: US/10/668,400
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: US 09/049,847
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: US 60/041,726
; PRIOR FILING DATE: 1997-03-27
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 11
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: Designed synthetic linear glycopeptide containing a
saccharidic
; OTHER INFORMATION: B-cell epitope and a CD4+ T-cell epitope able to induce
anti-
; OTHER INFORMATION: saccharidic antibodies
US-10-668-400-17
```

```
Query Match          27.3%; Score 3; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;
```

```
Qy          3 GGK 5
            |||
Db          8 GGK 10
```

# RESULT 69

```
US-10-668-400-18
; Sequence 18, Application US/10668400
; Publication No. US20040058859A1
; GENERAL INFORMATION:
; APPLICANT: Bay, Sylvie
; APPLICANT: Cantacuzene, Daniele
; APPLICANT: Leclerc, Claude
; APPLICANT: Lo-Man, Richard
; TITLE OF INVENTION: MULTIPLE ANTIGEN GLYCOPEPTIDE CARBOHYDRATE,
; TITLE OF INVENTION: VACCINE COMPRISING THE SAME AND USE THEREOF
; FILE REFERENCE: 102.166A-1
; CURRENT APPLICATION NUMBER: US/10/668,400
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: US 09/049,847
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: US 60/041,726
; PRIOR FILING DATE: 1997-03-27
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 11
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
```

```
; OTHER INFORMATION: Designed synthetic linear glycopeptide containing a
saccharidic
; OTHER INFORMATION: B-cell epitope and a CD4+ T-cell epitope able to induce
anti-
; OTHER INFORMATION: saccharidic antibodies
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(1)
; OTHER INFORMATION: alpha-N-acetylgalactosamine (GalNAc)-Serine
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (2)..(3)
; OTHER INFORMATION: alpha-N-acetylgalactosamine (GalNAc)-Threonine
US-10-668-400-18
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Query Match          27.3%; Score 3; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;
```

```
Qy          3 GGK 5
            |||
Db          8 GGK 10
```

#### RESULT 70

US-10-668-400-19

```
; Sequence 19, Application US/10668400
; Publication No. US20040058859A1
; GENERAL INFORMATION:
; APPLICANT: Bay, Sylvie
; APPLICANT: Cantacuzene, Daniele
; APPLICANT: Leclerc, Claude
; APPLICANT: Lo-Man, Richard
; TITLE OF INVENTION: MULTIPLE ANTIGEN GLYCOPEPTIDE CARBOHYDRATE,
; TITLE OF INVENTION: VACCINE COMPRISING THE SAME AND USE THEREOF
; FILE REFERENCE: 102.166A-1
; CURRENT APPLICATION NUMBER: US/10/668,400
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: US 09/049,847
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: US 60/041,726
; PRIOR FILING DATE: 1997-03-27
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 11
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: Designed synthetic linear glycopeptide containing a
saccharidic
; OTHER INFORMATION: B-cell epitope and a CD4+ T-cell epitope able to induce
anti-
; OTHER INFORMATION: saccharidic antibodies
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(1)
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; OTHER INFORMATION: alpha-N-acetylgalactosamine (GalNAc)-Serine  
; FEATURE:  
; NAME/KEY: MISC\_FEATURE  
; LOCATION: (2)..(3)  
; OTHER INFORMATION: alpha-N-acetylgalactosamine (GalNAc)-Threonine  
; FEATURE:  
; NAME/KEY: MISC\_FEATURE  
; LOCATION: (10)..(10)  
; OTHER INFORMATION: Biotinylated  
US-10-668-400-19

Query Match 27.3%; Score 3; DB 12; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GKK 5  
|||  
Db 8 GKK 10

RESULT 71

US-10-039-645-37  
; Sequence 37, Application US/10039645  
; Publication No. US20020147170A1  
; GENERAL INFORMATION:  
; APPLICANT: Kopin, Alan S.  
; APPLICANT: Beinborn, Martin  
; TITLE OF INVENTION: Constitutively Active, Hypersensitive,  
; TITLE OF INVENTION: and No. US20020147170A1functional Receptors as No.  
US20020147170A1el Therapeutic Agents  
; FILE REFERENCE: 00398/510002  
; CURRENT APPLICATION NUMBER: US/10/039,645  
; CURRENT FILING DATE: 2001-10-25  
; PRIOR APPLICATION NUMBER: US 60/243,550  
; PRIOR FILING DATE: 2000-10-26  
; NUMBER OF SEQ ID NOS: 87  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 37  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-039-645-37

Query Match 27.3%; Score 3; DB 13; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GKK 6  
|||  
Db 7 GKK 9

RESULT 72

US-10-165-015-32  
; Sequence 32, Application US/10165015  
; Publication No. US20030032594A1  
; GENERAL INFORMATION:

; APPLICANT: PACTT, Tech Transfer Office University of Lausanne  
; APPLICANT: Bonny, Christophe  
; TITLE OF INVENTION: INTRACELLULAR DELIVERY OF BIOLOGICAL EFFECTORS  
; FILE REFERENCE: 20349-512 CIP  
; CURRENT APPLICATION NUMBER: US/10/165,015  
; CURRENT FILING DATE: 2002-06-07  
; PRIOR APPLICATION NUMBER: 09/977,831  
; PRIOR FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: 60/240,315  
; PRIOR FILING DATE: 2000-10-13  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 32  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: TRANSPORTER  
; OTHER INFORMATION: PEPTIDE  
US-10-165-015-32

Query Match 27.3%; Score 3; DB 14; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GGK 5  
|||  
Db 2 GGK 4

RESULT 73  
US-10-108-795-26  
; Sequence 26, Application US/10108795  
; Publication No. US20030033633A1  
; GENERAL INFORMATION:  
; APPLICANT: Hemmings, Brian A  
; APPLICANT: Millward, Thomas A  
; TITLE OF INVENTION: Calcium Regulated Kinase  
; FILE REFERENCE: 30110  
; CURRENT APPLICATION NUMBER: US/10/108,795  
; CURRENT FILING DATE: 2002-03-28  
; PRIOR APPLICATION NUMBER: 09/133,062  
; PRIOR FILING DATE: 1998-08-12  
; PRIOR APPLICATION NUMBER: GB 9717089.8  
; PRIOR FILING DATE: 1997-08-12  
; PRIOR APPLICATION NUMBER: GB 9717499.9  
; PRIOR FILING DATE: 1998-08-19  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 26  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:synthetic peptide  
; OTHER INFORMATION: internal peptide  
US-10-108-795-26

Query Match 27.3%; Score 3; DB 14; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEG 3  
|||  
Db 9 AEG 11

RESULT 74

US-10-108-795-29

; Sequence 29, Application US/10108795  
; Publication No. US20030033633A1  
; GENERAL INFORMATION:  
; APPLICANT: Hemmings, Brian A  
; APPLICANT: Millward, Thomas A  
; TITLE OF INVENTION: Calcium Regulated Kinase  
; FILE REFERENCE: 30110  
; CURRENT APPLICATION NUMBER: US/10/108,795  
; CURRENT FILING DATE: 2002-03-28  
; PRIOR APPLICATION NUMBER: 09/133,062  
; PRIOR FILING DATE: 1998-08-12  
; PRIOR APPLICATION NUMBER: GB 9717089.8  
; PRIOR FILING DATE: 1997-08-12  
; PRIOR APPLICATION NUMBER: GB 9717499.9  
; PRIOR FILING DATE: 1998-08-19  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 29  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:synthetic peptide  
; OTHER INFORMATION: internal peptide  
US-10-108-795-29

Query Match 27.3%; Score 3; DB 14; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GKK 6  
|||  
Db 7 GKK 9

RESULT 75

US-10-039-831-11

; Sequence 11, Application US/10039831  
; Publication No. US20030044353A1  
; GENERAL INFORMATION:  
; APPLICANT: Weissleder, Ralph  
; APPLICANT: Tung, Ching-Hsuan  
; APPLICANT: Mahmood, Umar  
; TITLE OF INVENTION: ACTIVATABLE IMAGING PROBES  
; FILE REFERENCE: 00786-572001

; CURRENT APPLICATION NUMBER: US/10/039,831  
; CURRENT FILING DATE: 2002-01-04  
; PRIOR APPLICATION NUMBER: US 60/277,352  
; PRIOR FILING DATE: 2001-03-19  
; PRIOR APPLICATION NUMBER: US 60/260,123  
; PRIOR FILING DATE: 2001-01-05  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 11  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetically generated peptide  
; FEATURE:  
; NAME/KEY: VARIANT  
; LOCATION: (3)...(3)  
; OTHER INFORMATION: Xaa = pipecolic  
US-10-039-831-11

Query Match 27.3%; Score 3; DB 14; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GGK 5  
|||  
Db 8 GGK 10

Search completed: April 8, 2004, 16:35:48  
Job time : 31.3077 secs

OM protein - protein search, using sw model

Run on: April 8, 2004, 15:30:07 ; Search time 27.7692 Seconds  
(without alignments)  
124.984 Million cell updates/sec

Title: US-09-787-443A-19  
Perfect score: 11  
Sequence: 1 AEGGKKKKMRA 11

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 1017041 seqs, 315518202 residues

Word size : 0

Total number of hits satisfying chosen parameters: 460

Minimum DB seq length: 11  
Maximum DB seq length: 11

Post-processing: Listing first 100 summaries

Database : SPTREMBL\_25:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp Vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_rvirus:\*  
16: sp\_bacteriap:\*  
17: sp\_archeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result	%	Query					
No.	Score	Match	Length	DB	ID	Description	
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1	3	27.3	11	2	Q8RKN1	Q8rkn1 escherichia
2	3	27.3	11	10	Q9S8Z8	Q9s8z8 psophocarpu
3	3	27.3	11	13	Q9PS22	Q9ps22 xenopus lae
4	2	18.2	11	2	Q9R790	Q9r790 borrelia ga
5	2	18.2	11	2	Q9L4F7	Q9l4f7 bacillus ce
6	2	18.2	11	2	Q9S618	Q9s618 prochloroco
7	2	18.2	11	2	O87882	O87882 mycobacteri
8	2	18.2	11	2	Q8KTN1	Q8ktn1 candidatus
9	2	18.2	11	2	Q93MI7	Q93mi7 escherichia
10	2	18.2	11	2	Q9RFZ2	Q9rfz2 mycoplasma
11	2	18.2	11	2	P95518	P95518 pasteurella
12	2	18.2	11	2	Q47420	Q47420 escherichia
13	2	18.2	11	2	Q44090	Q44090 acholeplasm
14	2	18.2	11	2	Q8GMU3	Q8gmu3 acinetobact
15	2	18.2	11	2	Q9X9S6	Q9x9s6 streptomyce
16	2	18.2	11	2	Q7X566	Q7x566 thermus the
17	2	18.2	11	3	Q9UR95	Q9ur95 pichia angu
18	2	18.2	11	3	Q9URG1	Q9urg1 neurospora
19	2	18.2	11	3	Q96V15	Q96v15 cryptococcu
20	2	18.2	11	4	Q14759	Q14759 homo sapien
21	2	18.2	11	4	O60761	O60761 homo sapien
22	2	18.2	11	4	O75811	O75811 homo sapien
23	2	18.2	11	4	Q9H4H5	Q9h4h5 homo sapien
24	2	18.2	11	4	Q15997	Q15997 homo sapien
25	2	18.2	11	4	Q8NFN9	Q8nfn9 homo sapien
26	2	18.2	11	4	Q9UC46	Q9uc46 homo sapien
27	2	18.2	11	4	Q9UCR1	Q9ucr1 homo sapien
28	2	18.2	11	4	Q9UH72	Q9uh72 homo sapien
29	2	18.2	11	5	Q26092	Q26092 pisaster oc
30	2	18.2	11	5	Q9TWX6	Q9twx6 manduca sex
31	2	18.2	11	5	Q99292	Q99292 drosophila
32	2	18.2	11	5	Q9TWM2	Q9twm2 aplysia cal
33	2	18.2	11	5	Q8MM58	Q8mm58 heliconius
34	2	18.2	11	5	Q86D32	Q86d32 trypanosoma
35	2	18.2	11	5	Q86D31	Q86d31 trypanosoma
36	2	18.2	11	5	Q95PX6	Q95px6 caenorhabdi
37	2	18.2	11	6	Q9TRW5	Q9trw5 bos taurus
38	2	18.2	11	6	Q9TRX2	Q9trx2 bos taurus
39	2	18.2	11	6	Q9TQS9	Q9tqs9 equus cabal
40	2	18.2	11	7	O77892	O77892 oreochromis
41	2	18.2	11	7	O77880	O77880 oreochromis
42	2	18.2	11	7	O77906	O77906 oreochromis
43	2	18.2	11	7	O77893	O77893 oreochromis
44	2	18.2	11	7	O77907	O77907 oreochromis
45	2	18.2	11	8	Q9G5Y0	Q9g5y0 pseudotrape
46	2	18.2	11	8	Q9G356	Q9g356 agama atra
47	2	18.2	11	9	Q38415	Q38415 bacteriopha
48	2	18.2	11	9	Q37925	Q37925 bacteriopha
49	2	18.2	11	10	Q39784	Q39784 gossypium h
50	2	18.2	11	10	Q8RUE7	Q8rue7 zea mays (m
51	2	18.2	11	10	Q04131	Q04131 lycopersico
52	2	18.2	11	10	P82336	P82336 pisum sativ
53	2	18.2	11	11	Q99N81	Q99n81 mus musculu
54	2	18.2	11	11	Q9R1N6	Q9r1n6 mus musculu
55	2	18.2	11	11	Q9Z1H5	Q9z1h5 mus musculu
56	2	18.2	11	11	P81075	P81075 mus musculu
57	2	18.2	11	11	Q80WI3	Q80wi3 rattus sp.



58	2	18.2	11	12	Q83083	Q83083 leucania se
59	2	18.2	11	12	Q9J1G3	Q9j1g3 tt virus. o
60	2	18.2	11	12	O40974	O40974 cauliflower
61	2	18.2	11	13	Q8UUP1	Q8uup1 xenopus lae
62	2	18.2	11	13	Q8JGW8	Q8jgw8 ficedula al
63	2	18.2	11	13	Q90735	Q90735 gallus gall
64	2	18.2	11	15	Q98YS3	Q98ys3 human immun
65	2	18.2	11	15	P88018	P88018 human immun
66	1	9.1	11	2	Q9AIY6	Q9aiy6 carsonella
67	1	9.1	11	2	O68237	O68237 borrelia bu
68	1	9.1	11	2	Q48933	Q48933 mycobacteri
69	1	9.1	11	2	Q47451	Q47451 escherichia
70	1	9.1	11	2	Q9AIZ7	Q9aiz7 carsonella
71	1	9.1	11	2	Q52526	Q52526 rhizobium s
72	1	9.1	11	2	Q8KHL0	Q8kh10 streptococc
73	1	9.1	11	2	Q47602	Q47602 escherichia
74	1	9.1	11	2	Q47606	Q47606 escherichia
75	1	9.1	11	2	Q8L2T4	Q8l2t4 neisseria m
76	1	9.1	11	2	Q9R7U8	Q9r7u8 pseudomonas
77	1	9.1	11	2	Q9S623	Q9s623 prochloroco
78	1	9.1	11	2	Q9R5P3	Q9r5p3 serratia ma
79	1	9.1	11	2	P77404	P77404 escherichia
80	1	9.1	11	2	Q9RQ60	Q9rq60 buchnera ap
81	1	9.1	11	2	P96319	P96319 desulfovibr
82	1	9.1	11	2	Q93RM6	Q93rm6 staphylococ
83	1	9.1	11	2	Q9EUZ3	Q9euz3 escherichia
84	1	9.1	11	2	Q47600	Q47600 escherichia
85	1	9.1	11	2	Q8RMI8	Q8rmi8 enterococcu
86	1	9.1	11	2	Q9RBV0	Q9rbv0 pseudomonas
87	1	9.1	11	2	P71228	P71228 escherichia
88	1	9.1	11	2	Q9K332	Q9k332 staphylococ
89	1	9.1	11	2	Q47604	Q47604 escherichia
90	1	9.1	11	2	Q47345	Q47345 escherichia
91	1	9.1	11	2	Q9AIZ8	Q9aiz8 carsonella
92	1	9.1	11	2	Q8KRA1	Q8kra1 streptococc
93	1	9.1	11	2	Q47048	Q47048 escherichia
94	1	9.1	11	2	Q56413	Q56413 escherichia
95	1	9.1	11	2	Q47059	Q47059 escherichia
96	1	9.1	11	2	Q44237	Q44237 anabaena sp
97	1	9.1	11	2	Q9R872	Q9r872 escherichia
98	1	9.1	11	2	Q56972	Q56972 yersinia pe
99	1	9.1	11	2	Q9R446	Q9r446 neisseria g
100	1	9.1	11	2	Q91UY9	Q91uy9 escherichia

# ALIGNMENTS

## RESULT 1

Q8RKN1

ID Q8RKN1 PRELIMINARY; PRT; 11 AA.

AC Q8RKN1;

DT 01-JUN-2002 (TrEMBLrel. 21, Created)

DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)

DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)

DE Beta-lactamase CTX-M-9 (Fragment).

GN BLACTX-M-9.

OS *Escherichia coli*.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; *Escherichia*.  
 OX NCBI\_TaxID=562;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=743-D;  
 RA Sabate M., Navarro F., Miro E., Campoy S., Mirelis B., Barbe J.,  
 RA Prats G.;  
 RT "A novel complex sll-type integron in *Escherichia coli* carrying the  
 RT bla(CTX-M-9) gene."  
 RL Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AY092058; AAM15718.1; -.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 11 AA; 1071 MW; C26BF418D050440D CRC64;

Query Match 27.3%; Score 3; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 9.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEG 3  
 |||  
 Db 8 AEG 10

## RESULT 2

Q9S8Z8  
 ID Q9S8Z8 PRELIMINARY; PRT; 11 AA.  
 AC Q9S8Z8;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE W2 peptide (Fragment).  
 OS *Psophocarpus tetragonolobus* (Goa bean) (*Asparagus* bean).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;  
 OC *Psophocarpus*.  
 OX NCBI\_TaxID=3891;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=92232221; PubMed=1368037;  
 RA Hirano H., Kagawa H., Okubo K.;  
 RL *Phytochemistry* 31:731-735(1992).  
 FT NON\_TER 1 1  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1165 MW; 30487F18DABB42D7 CRC64;

Query Match 27.3%; Score 3; DB 10; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 9.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEG 3  
 |||  
 Db 8 AEG 10

# RESULT 3

Q9PS22

ID Q9PS22 PRELIMINARY; PRT; 11 AA.  
AC Q9PS22;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Hydrin 1', VASOTOCINYL-GLY-LYS.  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;  
OC Xenopodinae; Xenopus.  
OX NCBI\_TaxID=8355;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=93200145; PubMed=8452872;  
RA Iwamuro S., Hayashi H., Kikuyama S.;  
RT "An additional arginine-vasotocin-related peptide, vasotocinyl-Gly-  
RT Lys, in Xenopus neurohypophysis.";  
RL Biochim. Biophys. Acta 1176:143-147(1993).  
DR GO; GO:0005576; C:extracellular; IEA.  
DR GO; GO:0005185; F:neurohypophyseal hormone activity; IEA.  
DR InterPro; IPR000981; Neurhyp\_horm.  
DR Pfam; PF00220; hormone4; 1.  
DR PROSITE; PS00264; NEUROHYPOPHYS\_HORM; 1.  
SQ SEQUENCE 11 AA; 1238 MW; CC5B57EB176EB456 CRC64;

Query Match 27.3%; Score 3; DB 13; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GGK 5  
| | |  
Db 9 GGK 11

# RESULT 4

Q9R790

ID Q9R790 PRELIMINARY; PRT; 11 AA.  
AC Q9R790;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Outer surface protein C (Fragment).  
GN OSPC.  
OS Borrelia garinii.  
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.  
OX NCBI\_TaxID=29519;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=G25;  
RX MEDLINE=97426044; PubMed=9282748;  
RA Tilly K., Casjens S., Stevenson B., Bono J.L., Samuels D.S., Hogan D.,  
RA Rosa P.;  
RT "he Borrelia burgdorferi circular plasmid cp26: conservation of  
RT plasmid structure and targeted inactivation of the ospC gene.";  
RL Mol. Microbiol. 25:361-374(1997).

DR EMBL; U93700; AAC45535.1; -.  
DR GO; GO:0009279; C:external outer membrane (sensu Gram-negativ. . .; IEA.  
DR GO; GO:0003793; F:defense/immunity protein activity; IEA.  
DR GO; GO:0006952; P:defense response; IEA.  
DR InterPro; IPR001800; Lipoprotein\_6.  
DR Pfam; PF01441; Lipoprotein\_6; 1.  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1250 MW; 0868D864C5B731A4 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KK 6  
||  
Db 2 KK 3

RESULT 5

Q9L4F7

ID Q9L4F7 PRELIMINARY; PRT; 11 AA.  
AC Q9L4F7;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
DE Phosphatidylinositol-specific phospholipase C (PI-PLC)  
DE (Fragment).  
GN PLCA.  
OS Bacillus cereus.  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
OX NCBI\_TaxID=1396;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ATCC 14579 type strain;  
RX MEDLINE=20055637; PubMed=10589720;  
RA Okstad O., Gominet M., Purnelle B., Rose M., Lereclus D., Kolsto A.B.;  
RT "Sequence analysis of three Bacillus cereus loci under PlcR-regulated  
RT genes encoding degradative enzymes and enterotoxin."  
RL Microbiology 145:3129-3138(1999).  
DR EMBL; AJ243711; CAB69804.1; -.  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1335 MW; 4277A30E20572333 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KK 6  
||  
Db 4 KK 5

RESULT 6

Q9S618

ID Q9S618 PRELIMINARY; PRT; 11 AA.  
AC Q9S618;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)  
 DE Cytochrome b6/f complex subunit IV (Fragment).  
 GN PETD.  
 OS Prochlorococcus sp.  
 OC Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;  
 OC Prochlorococcus.  
 OX NCBI\_TaxID=1220;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Urbach E., Chisholm S.W.;  
 RT "Genetic diversity in Prochlorococcus populations flow cytometrically  
 RT sorted from the Sargasso Sea and Gulf Stream.";  
 RL Limnol. Oceanog. 43:1615-1630(1998).  
 DR EMBL; AF070132; AAD20740.1; -.  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1297 MW; 5CC38013B7633337 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KK 6  
 ||  
 Db 5 KK 6

#### RESULT 7

O87882

ID O87882 PRELIMINARY; PRT; 11 AA.  
 AC O87882;  
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)  
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
 DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)  
 DE Alkyl hydroperoxide reductase (Fragment).  
 GN AHPC.  
 OS Mycobacterium xenopi.  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
 OX NCBI\_TaxID=1789;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC19250;  
 RX MEDLINE=98406038; PubMed=9733688;  
 RA Pagan-Ramos E., Song J., McFalone M., Mudd M.H., Deretic V.;  
 RT "Oxidative stress response and characterization of the oxyR-ahpC and  
 RT furA-katG loci in Mycobacterium marinum.";  
 RL J. Bacteriol. 180:4856-4864(1998).  
 DR EMBL; U43810; AAC61663.1; -.  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1147 MW; 45458CE1787041A7 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GG 4

Db                    ||  
                      7 GG 8

RESULT 8

Q8KTN1

ID    Q8KTN1            PRELIMINARY;            PRT;        11 AA.  
AC    Q8KTN1;  
DT    01-OCT-2002 (TrEMBLrel. 22, Created)  
DT    01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT    01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE    Phosphoribosylpyrophosphate synthetase (Fragment).  
GN    PRS.  
OS    Candidatus Tremblaya princeps.  
OC    Bacteria; Proteobacteria; Betaproteobacteria; Candidatus Tremblaya.  
OX    NCBI\_TaxID=189385;  
RN    [1]  
RP    SEQUENCE FROM N.A.  
RX    MEDLINE=22083449; PubMed=12088995;  
RA    Baumann L., Thao M.L., Hess J.M., Johnson M.W., Baumann P.;  
RT    "The Genetic Properties of the Primary Endosymbionts of Mealybugs  
RT    Differ from Those of Other Endosymbionts of Plant Sap-Sucking  
RT    Insects.";  
RL    Appl. Environ. Microbiol. 68:3198-3205(2002).  
DR    EMBL; AF481911; AAM76018.1; -.  
FT    NON\_TER        11        11  
SQ    SEQUENCE    11 AA;    1127 MW;    4C127758A8676727 CRC64;

Query Match                    18.2%;    Score 2;    DB 2;    Length 11;  
Best Local Similarity        100.0%;    Pred. No. 1e+05;  
Matches        2;    Conservative        0;    Mismatches        0;    Indels        0;    Gaps        0;

Qy                    4 GK 5  
                      ||  
Db                    9 GK 10

RESULT 9

Q93MI7

ID    Q93MI7            PRELIMINARY;            PRT;        11 AA.  
AC    Q93MI7;  
DT    01-DEC-2001 (TrEMBLrel. 19, Created)  
DT    01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT    01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE    Adhesin (Fragment).  
GN    IHA.  
OS    Escherichia coli.  
OC    Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC    Enterobacteriaceae; Escherichia.  
OX    NCBI\_TaxID=562;  
RN    [1]  
RP    SEQUENCE FROM N.A.  
RC    STRAIN=CFT073;  
RA    Stoll A.L.;  
RL    Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.  
DR    EMBL; AF401752; AAK94916.1; -.  
FT    NON\_TER        11        11

SQ SEQUENCE 11 AA; 1203 MW; 8E2817ECBDD731B1 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 MR 10

||

Db 1 MR 2

RESULT 10

Q9RFZ2

ID Q9RFZ2 PRELIMINARY; PRT; 11 AA.

AC Q9RFZ2;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

DE Fructose biphosphate aldolase (Fragment).

GN FBA.

OS Mycoplasma mycoides subsp. capri.

OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.

OX NCBI\_TaxID=40477;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=PG3;

RX MEDLINE=20193983; PubMed=10727835;

RA Thiaucourt F., Lorenzon S., David A., Breard A.;

RT "Phylogeny of the Mycoplasma mycoides cluster as shown by sequencing  
of a putative membrane protein gene.";

RL Vet. Microbiol. 72:251-268(2000).

DR EMBL; AF162998; AAF15255.1; -.

FT NON TER 11 11

SQ SEQUENCE 11 AA; 1371 MW; 50B0881A3331FB57 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KK 6

||

Db 7 KK 8

RESULT 11

P95518

ID P95518 PRELIMINARY; PRT; 11 AA.

AC P95518;

DT 01-MAY-1997 (TrEMBLrel. 03, Created)

DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)

DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

DE Ribosomal protein RpsA (Fragment).

GN RPSA.

OS Pasteurella haemolytica.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;

OC Pasteurellaceae; Mannheimia.

OX NCBI\_TaxID=75985;

RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=PHL101;  
 RX MEDLINE=97164347; PubMed=9011038;  
 RA Highlander S.K., Garza O., Brown B.J., Koby S., Oppenheim A.B.;  
 RT "Isolation and characterization of the integration host factor genes  
 RT of *Pasteurella haemolytica*.";   
 RL FEMS Microbiol. Lett. 146:181-188(1997).  
 DR EMBL; U56139; AAC44845.1; -.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 11 AA; 1168 MW; 7A4BFD38D339CDDDB CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AE 2  
 ||  
 Db 3 AE 4

# RESULT 12

Q47420

ID Q47420 PRELIMINARY; PRT; 11 AA.  
 AC Q47420;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE ORF11 protein.  
 OS *Escherichia coli*.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; *Escherichia*.  
 OX NCBI\_TaxID=562;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=K12;  
 RX MEDLINE=92041688; PubMed=1657895;  
 RA Sharples G.J., Lloyd R.G.;  
 RT "Resolution of Holliday junctions in *Escherichia coli*: Identification  
 RT of the *ruvC* gene product as a 19-Kilodalton protein.";   
 RL J. Bacteriol. 173:7711-7715(1991).  
 DR EMBL; X59551; CAA42127.1; -.  
 DR PIR; S19015; S19015.  
 SQ SEQUENCE 11 AA; 1215 MW; DD8D6D4D56C6D33D CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 MR 10  
 ||  
 Db 1 MR 2

# RESULT 13

Q44090

ID Q44090 PRELIMINARY; PRT; 11 AA.



AC Q44090;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Hypothetical export segment (Fragment).  
 OS Acholeplasma laidlawii.  
 OC Bacteria; Firmicutes; Mollicutes; Acholeplasmatales;  
 OC Acholeplasmataceae; Acholeplasma.  
 OX NCBI\_TaxID=2148;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=A-EF22;  
 RA Boyer M.J., Jarhede T.K., Tegman V., Wieslander A.;  
 RT "Sequence regions from Acholeplasma laidlawii which restore export of  
 RT beta-lactamase in Escherichia coli.";  
 RL Submitted (JUN-1993) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; Z22875; CAA80495.1; -.  
 DR PIR; S33519; S33519.  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1234 MW; 5C9D2AE8A682C337 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KK 6  
 ||  
 Db 2 KK 3

#### RESULT 14

##### Q8GMU3

ID Q8GMU3 PRELIMINARY; PRT; 11 AA.  
 AC Q8GMU3;  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Putative catalase isozyme (Fragment).  
 GN KATA.  
 OS Acinetobacter lwoffii.  
 OG Plasmid pKLH202.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
 OC Moraxellaceae; Acinetobacter.  
 OX NCBI\_TaxID=28090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=TC108;  
 RA Kholodii G.Y., Yurieva O.V., Mindlin S.Z., Gorlenko Z.M.,  
 RA Nikiforov V.G.;  
 RT "pKLH2-like aberrant transposons and possible mechanisms of their  
 RT dissemination.";  
 RL Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AJ250245; CAC80800.1; -.  
 DR GO; GO:0046821; C:extrachromosomal DNA; IEA.  
 KW Plasmid.  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1233 MW; 81A15757B333276A CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KK 6  
||  
Db 6 KK 7

RESULT 15

Q9X9S6

ID Q9X9S6 PRELIMINARY; PRT; 11 AA.  
AC Q9X9S6;  
DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Hypothetical protein (Fragment).  
OS Streptomyces lividans.  
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
OC Streptomycineae; Streptomycetaceae; Streptomyces.  
OX NCBI\_TaxID=1916;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=TK21;  
RX MEDLINE=99328982; PubMed=10400594;  
RA Martinez-Costa O.H., Martin-Triana A.J., Martinez E.,  
RA Fernandez-Moreno M.A., Malpartida F.;  
RT "An additional regulatory gene for actinorhodin production in  
RT Streptomyces lividans involves a LysR-type transcriptional  
RT regulator.";  
RL J. Bacteriol. 181:4353-4364(1999).  
DR EMBL; Y18818; CAB51138.1; -.  
KW Hypothetical protein.  
FT NON\_TER 1 1  
SQ SEQUENCE 11 AA; 1160 MW; D1BABA8EG1EDC412 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 RA 11  
||  
Db 5 RA 6

RESULT 16

Q7X566

ID Q7X566 PRELIMINARY; PRT; 11 AA.  
AC Q7X566;  
DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Hypothetical protein (Fragment).  
OS Thermus thermophilus.  
OC Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;  
OC Thermus.

OX NCBI\_TaxID=274;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Miyazaki T., Miyazaki J., Nishiyama M., Yamane H.;  
 RT "Characterization of a LysN, the 4th enzyme in lysine biosynthesis, in  
 RT an extremely thermophilic bacterium, *Thermus thermophilus* HB27.";  
 RL Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AB097117; BAC76940.1; -.  
 KW Hypothetical protein.  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1073 MW; 39792C1E75B72EB8 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GG 4  
 ||  
 Db 3 GG 4

# RESULT 17

## Q9UR95

ID Q9UR95 PRELIMINARY; PRT; 11 AA.  
 AC Q9UR95;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)  
 DE Heat shock protein 60 homolog (Fragment).  
 OS *Pichia angusta* (Yeast) (*Hansenula polymorpha*).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; *Pichia*.  
 OX NCBI\_TaxID=4905;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=93223840; PubMed=8096822;  
 RA Evers M.E., Huhse B., Titorenko V.I., Kunau W.H., Hartl F.U.,  
 RA Harder W., Veenhuis M.;  
 RT "Affinity purification of molecular chaperones of the yeast *Hansenula*  
 RT *polymorpha* using immobilized denatured alcohol oxidase.";  
 RL FEBS Lett. 321:32-36(1993).  
 SQ SEQUENCE 11 AA; 1230 MW; 71872C1779C3372B CRC64;

Query Match 18.2%; Score 2; DB 3; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EG 3  
 ||  
 Db 10 EG 11

# RESULT 18

## Q9URG1

ID Q9URG1 PRELIMINARY; PRT; 11 AA.  
 AC Q9URG1;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE Cytochrome C oxidase subunit 2 (Fragment).  
 OS *Neurospora crassa*.  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 OC Sordariomycetidae; Sordariales; Sordariaceae; *Neurospora*.  
 OX NCBI\_TaxID=5141;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92035058; PubMed=1657411;  
 RA Lemire E.G., Percy J.A., Correia J.M., Crowther B.M., Nargang F.E.;  
 RT "Alteration of the cytochrome c oxidase subunit 2 gene in the [exn-5]  
 mutant of *Neurospora crassa*.";  
 RL Curr. Genet. 20:121-127(1991).  
 FT NON\_TER 1 1  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1222 MW; 936B1558C7605DC5 CRC64;

Query Match 18.2%; Score 2; DB 3; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EG 3  
 ||  
 Db 10 EG 11

#### RESULT 19

Q96V15

ID Q96V15 PRELIMINARY; PRT; 11 AA.  
 AC Q96V15;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Pheromone alpha (Fragment).  
 GN MFALPHA1A.  
 OS *Cryptococcus neoformans* var. *neoformans*.  
 OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;  
 OC Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.  
 OX NCBI\_TaxID=40410;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=IUM 98-3351;  
 RX MEDLINE=21538945; PubMed=11682503;  
 RA Cogliati M., Esposto M.C., Clarke D.L., Wickes B.L., Viviani M.A.;  
 RT "Origin of *Cryptococcus neoformans* var. *neoformans* Diploid Strains.";  
 RL J. Clin. Microbiol. 39:3889-3894(2001).  
 DR EMBL; AF377019; AAK55615.1; -.  
 FT NON\_TER 1 1  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1154 MW; C764AF6E786761ED CRC64;

Query Match 18.2%; Score 2; DB 3; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GG 4

Db                    ||  
                      7 GG 8

RESULT 20

Q14759

ID    Q14759            PRELIMINARY;            PRT;        11 AA.  
AC    Q14759;  
DT    01-NOV-1996 (TrEMBLrel. 01, Created)  
DT    01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT    01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE    Lymphocyte cytosolic protein 2 (Fragment).  
GN    LCP2.  
OS    Homo sapiens (Human).  
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX    NCBI\_TaxID=9606;  
RN    [1]  
RP    SEQUENCE FROM N.A.  
RA    Sunden S.L.F., Carr L.L., Clements J.L, Motto D.G., Koretzky G.A.;  
RT    "Polymorphism in and localization of the gene encoding the 76 kDa SH2  
RT    domain-containing Leukocyte Protein (SLP-76) to chromosome 5q33.1-  
RT    qter.";  
RL    Genomics 0:0-0(1995).  
DR    EMBL; U44065; AAA93308.1; -.  
FT    NON\_TER            1            1  
FT    NON\_TER            11           11  
SQ    SEQUENCE    11 AA;    1242 MW;    D695104224072DDD CRC64;

Query Match                    18.2%;    Score 2;    DB 4;    Length 11;  
Best Local Similarity        100.0%;    Pred. No. 1e+05;  
Matches        2;    Conservative        0;    Mismatches        0;    Indels        0;    Gaps        0;

Qy                    1 AE 2  
                      ||  
Db                    2 AE 3

RESULT 21

O60761

ID    O60761            PRELIMINARY;            PRT;        11 AA.  
AC    O60761;  
DT    01-AUG-1998 (TrEMBLrel. 07, Created)  
DT    01-AUG-1998 (TrEMBLrel. 07, Last sequence update)  
DT    01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE    NPT-1 protein (Fragment).  
GN    NPT-1.  
OS    Homo sapiens (Human).  
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX    NCBI\_TaxID=9606;  
RN    [1]  
RP    SEQUENCE FROM N.A.  
RX    MEDLINE=98207718; PubMed=9545579;  
RA    Taketani Y., Miyamoto K., Chikamori M., Tanaka K., Yamamoto H.,  
RA    Tatsumi S., Morita K., Takeda E.;  
RT    "Characterization of the 5' flanking region of the human NPT-1

RT Na+/phosphate cotransporter gene.";  
RL Biochim. Biophys. Acta 1396:267-272(1998).  
DR EMBL; D83236; BAA25645.1; -.  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1358 MW; 884E2D4E6734044A CRC64;

Query Match 18.2%; Score 2; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KK 6  
||  
Db 10 KK 11

RESULT 22  
O75811

ID O75811 PRELIMINARY; PRT; 11 AA.  
AC O75811;  
DT 01-NOV-1998 (TrEMBLrel. 08, Created)  
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)  
DE ErbB-3 R2 (Fragment).  
GN C-ERBB-3.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Ovarian carcinoma;  
RX MEDLINE=98345147; PubMed=9681822;  
RA Lee H., Maihle N.J.;  
RT "Isolation and characterization of four alternate c-erbB3 transcripts  
RT expressed in ovarian carcinoma-derived cell lines and normal human  
RT tissues.";  
RL Oncogene 16:3243-3252(1998).  
DR EMBL; U88358; AAC39858.1; -.  
FT NON\_TER 1 1  
SQ SEQUENCE 11 AA; 1017 MW; 21B236366EB72878 CRC64;

Query Match 18.2%; Score 2; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GG 4  
||  
Db 4 GG 5

RESULT 23  
Q9H4H5

ID Q9H4H5 PRELIMINARY; PRT; 11 AA.  
AC Q9H4H5;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)

DE DJ661I20.2 (Novel helicase C-terminal domain and SNF2 N-terminal  
 DE domains containing protein) (Fragment).  
 GN DJ620E11.1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Skuce C.;  
 RL Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AL031669; CAC17164.2; -.  
 FT NON\_TER 1 1  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1420 MW; 5EB2C32A3326D053 CRC64;

Query Match 18.2%; Score 2; DB 4; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KM 9  
 ||  
 Db 2 KM 3

#### RESULT 24

Q15997

ID Q15997 PRELIMINARY; PRT; 11 AA.  
 AC Q15997;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE RARA protein (Fragment).  
 GN RARA.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93222087; PubMed=7682097;  
 RA Dong S., Geng J.P., Tong J.H., Wu Y., Cai J.R., Sun G.L., Chen S.R.,  
 RA Wang Z.Y., Larsen C.J., Berger R., et al;  
 RT "Breakpoint clusters of the PML gene in acute promyelocytic leukemia:  
 RT primary structure of the reciprocal products of the PML-RARA gene in a  
 RT patient with t(15;17).";  
 RL Genes Chromosomes Cancer 6:133-139(1993).  
 DR EMBL; S57794; AAD13888.1; -.  
 DR PIR; I54081; I54081.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 11 AA; 1277 MW; 33C70E22CDDDC417 CRC64;

Query Match 18.2%; Score 2; DB 4; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 RA 11

Db                    ||  
                      5 RA 6

RESULT 25

Q8NFN9

ID    Q8NFN9            PRELIMINARY;            PRT;        11 AA.  
AC    Q8NFN9;  
DT    01-OCT-2002 (TrEMBLrel. 22, Created)  
DT    01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT    01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE    Corticotropin releasing hormone receptor 1 (Fragment).  
GN    CRHR1.  
OS    Homo sapiens (Human).  
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX    NCBI\_TaxID=9606;  
RN    [1]  
RP    SEQUENCE FROM N.A.  
RA    Parham K.L., Catalano R., Hillhouse E.W.;  
RT    "Identification of the Promoter Region of the Human Type 1 CRH  
RT    Receptor Gene."  
RL    Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.  
DR    EMBL; AF488558; AAM55213.1; -.  
DR    GO; GO:0004872; F:receptor activity; IEA.  
KW    Receptor.  
FT    NON\_TER            11            11  
SQ    SEQUENCE    11 AA;    1236 MW;    ECEE030D0736C761 CRC64;

Query Match                    18.2%;    Score 2;    DB 4;    Length 11;  
Best Local Similarity    100.0%;    Pred. No. 1e+05;  
Matches        2;    Conservative        0;    Mismatches        0;    Indels        0;    Gaps        0;

Qy                    3 GG 4  
                      ||  
Db                    2 GG 3

RESULT 26

Q9UC46

ID    Q9UC46            PRELIMINARY;            PRT;        11 AA.  
AC    Q9UC46;  
DT    01-MAY-2000 (TrEMBLrel. 13, Created)  
DT    01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT    01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE    Neutrophil inhibitor peptide, NIP=POLYMORPHONUCLEAR neutrophil  
DE    inhibitor peptide.  
OS    Homo sapiens (Human).  
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX    NCBI\_TaxID=9606;  
RN    [1]  
RP    SEQUENCE.  
RX    MEDLINE=96326114; PubMed=8703476;  
RA    Cooper J.A.Jr., Culbreth R.R.;  
RT    "Characterization of a neutrophil inhibitor peptide harvested from  
RT    human bronchial lavage: homology to influenza A nucleoprotein.";



RL Am. J. Respir. Cell Mol. Biol. 15:207-215(1996).  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0030236; P:anti-inflammatory response; NAS.  
SQ SEQUENCE 11 AA; 1262 MW; 951A1C3279C9DB45 CRC64;

Query Match 18.2%; Score 2; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EG 3  
||  
Db 2 EG 3

#### RESULT 27

##### Q9UCR1

ID Q9UCR1 PRELIMINARY; PRT; 11 AA.  
AC Q9UCR1;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE AUTOTAXIN (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=92129337; PubMed=1733949;  
RA Stracke M.L., Krutzsch H.C., Unsworth E.J., Arestad A., Cioce V.,  
RA Schiffmann E., Liotta L.A.;  
RT "Identification, purification, and partial sequence analysis of  
RT autotaxin, a novel motility-stimulating protein.";  
RL J. Biol. Chem. 267:2524-2529(1992).  
FT NON\_TER 1 1  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1171 MW; 2723615AA0437737 CRC64;

Query Match 18.2%; Score 2; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GG 4  
||  
Db 1 GG 2

#### RESULT 28

##### Q9UH72

ID Q9UH72 PRELIMINARY; PRT; 11 AA.  
AC Q9UH72;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE V1-vascular vasopressin receptor AVPR1A (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Thibonnier M., Willard H.F., Jeunemaitre X.;  
 RT "Study of V1-vascular vasopressin receptor gene microsatellite  
 RT polymorphisms in human essential hypertension.";  
 RL Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AF208541; AAF18470.1; -.  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 KW Receptor.  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1071 MW; 8653B8E3B7687DC5 CRC64;

Query Match 18.2%; Score 2; DB 4; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 MR 10  
 ||  
 Db 1 MR 2

#### RESULT 29

Q26092

ID Q26092 PRELIMINARY; PRT; 11 AA.  
 AC Q26092;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Sea STAR histone H2B gene 5'region (Fragment).  
 OS Pisaster ochraceus (Sea star).  
 OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Asterozoa;  
 OC Asteroidea; Forcipulatacea; Forcipulatida; Asteriidae; Pisaster.  
 OX NCBI\_TaxID=7612;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Sperm;  
 RA Howell A.M., Cool D., Hewitt J., Ydenberg B., Smith M.J., Honda B.M.;  
 RT "Organization and Unusual Expression of Histone Genes in the Sea Star  
 RT Pisaster ochraceus.";  
 RL J. Mol. Evol. 25:29-36(1987).  
 DR EMBL; X05619; CAA29106.1; -.  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1128 MW; 5173974A3865BDD3 CRC64;

Query Match 18.2%; Score 2; DB 5; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GK 5  
 ||  
 Db 7 GK 8

#### RESULT 30

Q9Twx6

ID Q9TWX6 PRELIMINARY; PRT; 11 AA.  
AC Q9TWX6;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Juvenile hormone binding protein, JHBP=12.5 kDa CNBR peptide  
DE (Fragment).  
OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Sphingioidea;  
OC Sphingidae; Sphinginae; Manduca.  
OX NCBI\_TaxID=7130;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=92134256; PubMed=1734862;  
RA Touhara K., Prestwich G.D.;  
RT "Binding site mapping of a photoaffinity-labeled juvenile hormone  
RT binding protein.";  
RL Biochem. Biophys. Res. Commun. 182:466-473(1992).  
FT NON\_TER 1 1  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1071 MW; D232A98E705045BD CRC64;

Query Match 18.2%; Score 2; DB 5; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GG 4  
||  
Db 8 GG 9

RESULT 31  
Q99292  
ID Q99292 PRELIMINARY; PRT; 11 AA.  
AC Q99292;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Bicoid protein (Fragment).  
GN BCD.  
OS Drosophila heteroneura (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=32382;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=91184004; PubMed=2081457;  
RA MacDonald P.M.;  
RT "bicoid mRNA localization signal: phylogenetic conservation of  
RT function and RNA secondary structure.";  
RL Development 110:161-171(1990).  
CC -!- FUNCTION: BICOID IS SEGMENT-POLARITY PROTEIN THAT PROVIDES  
CC POSITIONAL CUES FOR THE DEVELOPMENT OF HEAD AND THORACIC SEGMENTS.  
CC BCD REGULATES THE EXPRESSION OF ZYGOTIC GENES, POSSIBLY THROUGH  
CC ITS HOMEODOMAIN, AND INHIBITS THE ACTIVITY OF OTHER MATERNAL GENE

CC PRODUCTS. IT IS POSSIBLE THAT BCD ALSO BINDS RNA.  
 DR EMBL; M32125; AAA28386.1; -.  
 DR FlyBase; FBgn0012352; Dhet\bcd.  
 DR GO; GO:0005634; C:nucleus; IEA.  
 DR GO; GO:0003677; F:DNA binding; IEA.  
 DR GO; GO:0003723; F:RNA binding; IEA.  
 DR GO; GO:0007275; P:development; IEA.  
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
 DR GO; GO:0007367; P:segment polarity determination; IEA.  
 KW DNA-binding; Developmental protein; Homeobox; Nuclear protein;  
 KW RNA-binding; Segmentation polarity protein; Transcription regulation.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 11 AA; 1221 MW; 8CE802305DD9D6C1 CRC64;

Query Match 18.2%; Score 2; DB 5; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GG 4  
 ||  
 Db 1 GG 2

# RESULT 32

Q9TWM2

ID Q9TWM2 PRELIMINARY; PRT; 11 AA.  
 AC Q9TWM2;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)  
 DE Buccalin B, BUCB.  
 OS Aplysia californica (California sea hare).  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;  
 OC Apogastropoda; Heterobranchia; Euthyneura; Opisthobranchia; Anaspidea;  
 OC Aplysioidea; Aplysiidae; Aplysia.  
 OX NCBI\_TaxID=6500;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=95083478; PubMed=7991459;  
 RA Vilim F.S., Cropper E.C., Rosen S.C., Tenenbaum R., Kupfermann I.,  
 RA Weiss K.R.;  
 RT "Structure, localization, and action of buccalin B: a bioactive  
 RT peptide from Aplysia."  
 RL Peptides 15:959-969(1994).  
 SQ SEQUENCE 11 AA; 1153 MW; 692253F9C9C86B44 CRC64;

Query Match 18.2%; Score 2; DB 5; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GG 4  
 ||  
 Db 9 GG 10

# RESULT 33

Q8MM58

ID Q8MM58 PRELIMINARY; PRT; 11 AA.  
AC Q8MM58;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Mannose phosphate isomerase (Fragment).  
GN MPI.  
OS Heliconius cydno chioneus.  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;  
OC Papilionoidea; Nymphalidae; Heliconiinae; Heliconius.  
OX NCBI\_TaxID=171915;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=STRI-B-553-Mpi-1, and STRI-B-553-Mpi-2;  
RA Bull V., Beltran M., Bermingham E., Jiggins C., McMillan O.,  
RA Mallet J.;  
RT "Molecular evidence for gene flow between species of Heliconius."  
RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; AF516222; AAM61908.1; -.  
DR EMBL; AF516223; AAM61909.1; -.  
DR GO; GO:0016853; F:isomerase activity; IEA.  
KW Isomerase.  
FT NON\_TER 1 1  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1312 MW; 56A67DB31DD1EAA3 CRC64;

Query Match 18.2%; Score 2; DB 5; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AE 2  
||  
Db 7 AE 8

# RESULT 34

Q86D32  
ID Q86D32 PRELIMINARY; PRT; 11 AA.  
AC Q86D32;  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Histone H1 (Fragment).  
OS Trypanosoma cruzi.  
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.  
OX NCBI\_TaxID=5693;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Dm28c;  
RX MEDLINE=22557728; PubMed=12670512;  
RA Sturm N.R., Vargas N.S., Westenberger S.J., Zingales B.,  
RA Campbell D.A.;  
RT "Evidence for multiple hybrid groups in Trypanosoma cruzi."  
RL Int. J. Parasitol. 33:269-279(2003).  
DR EMBL; AF545075; AAP21903.1; -.  
FT NON\_TER 11 11

SQ SEQUENCE 11 AA; 1114 MW; CCC1B31E7772CDDD CRC64;

Query Match 18.2%; Score 2; DB 5; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KK 6  
||  
Db 9 KK 10

RESULT 35

Q86D31

ID Q86D31 PRELIMINARY; PRT; 11 AA.  
AC Q86D31;  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Histone H1 (Fragment).  
OS Trypanosoma cruzi.  
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.  
OX NCBI\_TaxID=5693;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Sylvio X10;  
RX MEDLINE=22557728; PubMed=12670512;  
RA Sturm N.R., Vargas N.S., Westenberger S.J., Zingales B.,  
RA Campbell D.A.;  
RT "Evidence for multiple hybrid groups in Trypanosoma cruzi."  
RL Int. J. Parasitol. 33:269-279(2003).  
DR EMBL; AF545076; AAP21906.1; -.  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1174 MW; CCD1B21E7772CDDD CRC64;

Query Match 18.2%; Score 2; DB 5; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KK 6  
||  
Db 9 KK 10

RESULT 36

Q95PX6

ID Q95PX6 PRELIMINARY; PRT; 11 AA.  
AC Q95PX6;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Hypothetical protein.  
GN ZK1236.8.  
OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
OC Rhabditidae; Peloderinae; Caenorhabditis.  
OX NCBI\_TaxID=6239;  
RN [1]

RP SEQUENCE FROM N.A.  
 RC STRAIN=Bristol N2;  
 RX MEDLINE=99069613; PubMed=9851916;  
 RA None;  
 RT "Genome sequence of the nematode C. elegans: a platform for  
 RT investigating biology. The C. elegans Sequencing Consortium.";  
 RL Science 282:2012-2018(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Bristol N2;  
 RA Favello A.;  
 RT "The sequence of C. elegans cosmid ZK1236.";  
 RL Submitted (MAY-1993) to the EMBL/GenBank/DDBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Bristol N2;  
 RA Waterston R.;  
 RT "Direct Submission.";  
 RL Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; L13200; AAL11108.1; -.  
 DR WormPep; ZK1236.8; CE29629.  
 KW Hypothetical protein.  
 SQ SEQUENCE 11 AA; 1304 MW; DFA3510A25A76322 CRC64;

Query Match 18.2%; Score 2; DB 5; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KK 6  
 ||  
 Db 8 KK 9

# RESULT 37

Q9TRW5

ID Q9TRW5 PRELIMINARY; PRT; 11 AA.  
 AC Q9TRW5;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE 25 kDa protein P25, peptide F4 (Fragment).  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=91372400; PubMed=1909972;  
 RA Takahashi M., Tomizawa K., Ishiguro K., Sato K., Omori A., Sato S.,  
 RA Shiratsuchi A., Uchida T., Imahori K.;  
 RT "A novel brain-specific 25 kDa protein (p25) is phosphorylated by a  
 RT Ser/Thr-Pro kinase (TPK II) from tau protein kinase fractions.";  
 RL FEBS Lett. 289:37-43(1991).  
 FT NON\_TER 1 1  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1276 MW; CAF72DAF65A76AA9 CRC64;

Query Match 18.2%; Score 2; DB 6; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GK 5  
||  
Db 10 GK 11

RESULT 38

Q9TRX2

ID Q9TRX2 PRELIMINARY; PRT; 11 AA.  
AC Q9TRX2;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Glutamate dehydrogenase (EC 1.4.1.3) (Fragment).  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;  
OC Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=91308094; PubMed=1854724;  
RA Ozturk D.H., Colman R.F.;  
RT "Identification of cysteine-319 as the target amino acid of 8-[(4-  
RT bromo-2,3-dioxobutyl)thio]adenosine 5'-triphosphate in bovine liver  
RT glutamate dehydrogenase.";  
RL Biochemistry 30:7126-7134(1991).  
DR GO; GO:0004353; F:glutamate dehydrogenase [NAD(P)] activity; IEA.  
SQ SEQUENCE 11 AA; 1207 MW; F46BF756A771B401 CRC64;

Query Match 18.2%; Score 2; DB 6; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GG 4  
||  
Db 10 GG 11

RESULT 39

Q9TQS9

ID Q9TQS9 PRELIMINARY; PRT; 11 AA.  
AC Q9TQS9;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)  
DE Transferrin (Fragment).  
OS Equus caballus (Horse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.  
OX NCBI\_TaxID=9796;  
RN [1]  
RP SEQUENCE FROM N.A.



RA Giffard J.M., Brandon R.B., Bell T.K.;  
 RT "Further identification of single nucleotide polymorphisms in the  
 RT equine transferrin gene."  
 RL Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AF185800; AAF05495.1; -.  
 DR EMBL; AF185797; AAF05492.1; -.  
 DR EMBL; AF185798; AAF05493.1; -.  
 DR EMBL; AF185799; AAF05494.1; -.  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1231 MW; C586121E2DC4005D CRC64;

Query Match 18.2%; Score 2; DB 6; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 MR 10  
 ||  
 Db 1 MR 2

#### RESULT 40

O77892  
 ID O77892 PRELIMINARY; PRT; 11 AA.  
 AC O77892;  
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)  
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE MHC class II B locus 10 (Fragment).  
 OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidei;  
 OC Cichlidae; Oreochromis.  
 OX NCBI\_TaxID=8128;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98315113; PubMed=9649539;  
 RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,  
 RA Figueroa F., Sultmann H., Klein J.;  
 RT "Linkage relationships and haplotype polymorphism among cichlid mhc  
 RT class II B loci."  
 RL Genetics 149:1527-1537(1998).  
 DR EMBL; AF050002; AAC41341.1; -.  
 FT NON\_TER 1 1  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1277 MW; 74855B73786B572B CRC64;

Query Match 18.2%; Score 2; DB 7; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GG 4  
 ||  
 Db 7 GG 8

#### RESULT 41

O77880

ID O77880 PRELIMINARY; PRT; 11 AA.  
AC O77880;  
DT 01-NOV-1998 (TrEMBLrel. 08, Created)  
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE MHC class II B locus 2 (Fragment).  
OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidae;  
OC Cichlidae; Oreochromis.  
OX NCBI\_TaxID=8128;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98315113; PubMed=9649539;  
RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,  
RA Figueroa F., Sultmann H., Klein J.;  
RT "Linkage relationships and haplotype polymorphism among cichlid mhc  
RT class II B loci.";  
RL Genetics 149:1527-1537(1998).  
DR EMBL; AF049989; AAC41328.1; -.  
FT NON\_TER 1 1  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1346 MW; AB5F2D9822D2DB56 CRC64;

Query Match 18.2%; Score 2; DB 7; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KM 9  
||  
Db 3 KM 4

RESULT 42

O77906

ID O77906 PRELIMINARY; PRT; 11 AA.  
AC O77906;  
DT 01-NOV-1998 (TrEMBLrel. 08, Created)  
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE MHC class II B locus 1 (Fragment).  
OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidae;  
OC Cichlidae; Oreochromis.  
OX NCBI\_TaxID=8128;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98315113; PubMed=9649539;  
RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,  
RA Figueroa F., Sultmann H., Klein J.;  
RT "Linkage relationships and haplotype polymorphism among cichlid mhc  
RT class II B loci.";  
RL Genetics 149:1527-1537(1998).

DR EMBL; AF050016; AAC41355.1; -.

FT NON\_TER 1 1

FT NON\_TER 11 11

SQ SEQUENCE 11 AA; 1277 MW; 74855B73786B572B CRC64;

Query Match 18.2%; Score 2; DB 7; Length 11;

Best Local Similarity 100.0%; Pred. No. 1e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GG 4

||

Db 7 GG 8

#### RESULT 43

O77893

ID O77893 PRELIMINARY; PRT; 11 AA.

AC O77893;

DT 01-NOV-1998 (TrEMBLrel. 08, Created)

DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)

DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

DE MHC class II B locus 10 (Fragment).

OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidei;

OC Cichlidae; Oreochromis.

OX NCBI\_TaxID=8128;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=98315113; PubMed=9649539;

RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,

RA Figueroa F., Sultmann H., Klein J.;

RT "Linkage relationships and haplotype polymorphism among cichlid mhc

RT class II B loci.";

RL Genetics 149:1527-1537(1998).

DR EMBL; AF050003; AAC41342.1; -.

FT NON\_TER 1 1

FT NON\_TER 11 11

SQ SEQUENCE 11 AA; 1296 MW; 68775B73786B572B CRC64;

Query Match 18.2%; Score 2; DB 7; Length 11;

Best Local Similarity 100.0%; Pred. No. 1e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GG 4

||

Db 7 GG 8

#### RESULT 44

O77907

ID O77907 PRELIMINARY; PRT; 11 AA.

AC O77907;

DT 01-NOV-1998 (TrEMBLrel. 08, Created)

DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)

DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

DE MHC class II B locus 2 (Fragment).  
 OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidei;  
 OC Cichlidae; Oreochromis.  
 OX NCBI\_TaxID=8128;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98315113; PubMed=9649539;  
 RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,  
 RA Figueroa F., Sultmann H., Klein J.;  
 RT "Linkage relationships and haplotype polymorphism among cichlid mhc  
 RT class II B loci."  
 RL Genetics 149:1527-1537(1998).  
 DR EMBL; AF050018; AAC41357.1; -.  
 FT NON\_TER 1 1  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1346 MW; AB5F2D9822D2DB56 CRC64;

Query Match 18.2%; Score 2; DB 7; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KM 9  
 ||  
 Db 3 KM 4

#### RESULT 45

Q9G5Y0

ID Q9G5Y0 PRELIMINARY; PRT; 11 AA.  
 AC Q9G5Y0;  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Cytochrome c oxidase subunit I (Fragment).  
 GN COI.  
 OS Pseudotrapelus sinaitus.  
 OG Mitochondrion.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Agaminae;  
 OC Pseudotrapelus.  
 OX NCBI\_TaxID=118229;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22114082; PubMed=12118408;  
 RA Macey J.R., Schulte J.A. II, Larson A.;  
 RT "Evolution and information content of the mitochondrial genomic  
 RT structural features illustrated with acrodont lizards."  
 RL Syst. Biol. 49:257-277(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22114081; PubMed=12118407;  
 RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,  
 RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;  
 RT "Evaluating Trans-Tethys migration: An example using Acrodont lizard

RT phylogenetics.";  
 RL Syst. Biol. 49:233-256(2000).  
 DR EMBL; AF128507; AAG00758.1; -.  
 DR GO; GO:0005739; C:mitochondrion; IEA.  
 KW Mitochondrion.  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1374 MW; B05439FE336415B6 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KM 9  
 ||  
 Db 3 KM 4

# RESULT 46

Q9G356

ID Q9G356 PRELIMINARY; PRT; 11 AA.  
 AC Q9G356;  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Cytochrome c oxidase subunit I (Fragment).  
 GN COI.  
 OS Agama atra (Southern rock agama).  
 OG Mitochondrion.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Agaminae; Agama.  
 OX NCBI\_TaxID=52208;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97153820; PubMed=9000751;  
 RA Macey J.R., Larson A., Ananjeva N.B., Papenfuss T.J.;  
 RT "Replication slippage may cause parallel evolution in the secondary  
 RT structures of mitochondrial transfer RNAs."  
 RL Mol. Biol. Evol. 14:30-39(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22114082; PubMed=12118408;  
 RA Macey J.R., Schulte J.A. II, Larson A.;  
 RT "Evolution and information content of the mitochondrial genomic  
 RT structural features illustrated with acrodont lizards."  
 RL Syst. Biol. 49:257-277(2000).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22114081; PubMed=12118407;  
 RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,  
 RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;  
 RT "Evaluating Trans-Tethys migration: An example using Acrodont lizard  
 RT phylogenetics."  
 RL Syst. Biol. 49:233-256(2000).  
 DR EMBL; AF128505; AAG00752.1; -.  
 DR GO; GO:0005739; C:mitochondrion; IEA.  
 KW Mitochondrion.  
 FT NON\_TER 11 11

SQ SEQUENCE 11 AA; 1402 MW; B052EC10D36411A6 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KM 9

||

Db 3 KM 4

RESULT 47

Q38415

ID Q38415 PRELIMINARY; PRT; 11 AA.

AC Q38415;

DT 01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE Ant1 protein (Fragment).

OS Bacteriophage P7.

OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;

OC P1-like viruses.

OX NCBI\_TaxID=10682;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=90335968; PubMed=1696181;

RA Citron M., Schuster H.;

RT "The c4 repressors of bacteriophages P1 and P7 are antisense RNAs.";

RL Cell 62:591-598(1990).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=92319637; PubMed=1620606;

RA Citron M., Schuster H.;

RT "The c4 repressor of bacteriophage P1 is a processed 77 base antisense

RNA.";

RL Nucleic Acids Res. 20:3085-3090(1992).

DR EMBL; M35139; AAA32437.1; -.

DR PIR; S42449; S42449.

FT NON\_TER 11 11

SQ SEQUENCE 11 AA; 1315 MW; 38A55C6D11B2C737 CRC64;

Query Match 18.2%; Score 2; DB 9; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KK 6

||

Db 2 KK 3

RESULT 48

Q37925

ID Q37925 PRELIMINARY; PRT; 11 AA.

AC Q37925;

DT 01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

DE Bacteriophage fr replicase (Fragment).  
 OS Bacteriophage fr.  
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;  
 OC Levivirus.  
 OX NCBI\_TaxID=12017;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Berzin V.M., Griбанov V.A., Cielens I.E., Jansone I.V., Gren E.J.;  
 RT "The nucleotide sequence of the regulatory region of phage fr  
 RT replicase cistron."  
 RL Bioorg. Khim. 7:306-308(1981).  
 DR EMBL; M34834; AAA32193.1; -.  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1285 MW; 8BD43470C33321B1 CRC64;

Query Match 18.2%; Score 2; DB 9; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KK 6  
 ||  
 Db 6 KK 7

#### RESULT 49

Q39784

ID Q39784 PRELIMINARY; PRT; 11 AA.  
 AC Q39784;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last annotation update)  
 DE Alcohol dehydrogenase 2b-2 (Fragment).  
 OS Gossypium hirsutum (Upland cotton).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.  
 OX NCBI\_TaxID=3635;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Blue Tag Siokra;  
 RA Millar A.A., Dennis E.S.;  
 RL Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; U53705; AAA98988.1; -.  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1161 MW; D67F443942D6D87D CRC64;

Query Match 18.2%; Score 2; DB 10; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 RA 11  
 ||  
 Db 9 RA 10

#### RESULT 50

Q8RUE7

ID Q8RUE7 PRELIMINARY; PRT; 11 AA.  
 AC Q8RUE7;  
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE Alcohol dehydrogenase (Fragment).  
 GN ADH1.  
 OS Zea mays (Maize).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC PACCAD clade; Panicoideae; Andropogoneae; Zea.  
 OX NCBI\_TaxID=4577;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Various strains;  
 RA Ching A.S., Caldwell K.S., Jung M., Dolan M., Smith O.S., Tingey S.,  
 RA Morgante M., Rafalski J.A.;  
 RT "SNP frequency, haplotype structure and linkage disequilibrium in  
 RT elite maize inbred lines."  
 RL Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AF496880; AAM16120.1; -.  
 DR EMBL; AF496881; AAM16121.1; -.  
 DR EMBL; AF496882; AAM16122.1; -.  
 DR EMBL; AF496883; AAM16123.1; -.  
 DR EMBL; AF496884; AAM16124.1; -.  
 DR EMBL; AF496885; AAM16125.1; -.  
 DR EMBL; AF496886; AAM16126.1; -.  
 DR EMBL; AF496887; AAM16127.1; -.  
 DR EMBL; AF496888; AAM16128.1; -.  
 DR EMBL; AF496889; AAM16129.1; -.  
 DR EMBL; AF496890; AAM16130.1; -.  
 DR EMBL; AF496891; AAM16131.1; -.  
 DR EMBL; AF496892; AAM16132.1; -.  
 DR EMBL; AF496893; AAM16133.1; -.  
 DR EMBL; AF496894; AAM16134.1; -.  
 DR EMBL; AF496895; AAM16135.1; -.  
 DR EMBL; AF496896; AAM16136.1; -.  
 DR EMBL; AF496897; AAM16137.1; -.  
 DR EMBL; AF496898; AAM16138.1; -.  
 DR EMBL; AF496899; AAM16139.1; -.  
 DR EMBL; AF496900; AAM16140.1; -.  
 DR EMBL; AF496901; AAM16141.1; -.  
 DR EMBL; AF496902; AAM16142.1; -.  
 DR EMBL; AF496903; AAM16143.1; -.  
 DR EMBL; AF496904; AAM16144.1; -.  
 DR EMBL; AF496905; AAM16145.1; -.  
 DR EMBL; AF496906; AAM16146.1; -.  
 DR EMBL; AF496907; AAM16147.1; -.  
 DR EMBL; AF496908; AAM16148.1; -.  
 DR EMBL; AF496909; AAM16149.1; -.  
 DR EMBL; AF496910; AAM16150.1; -.  
 DR EMBL; AF496911; AAM16151.1; -.  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1149 MW; D66AE90942C3387D CRC64;

Query Match 18.2%; Score 2; DB 10; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1e+05;



Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GK 5  
||  
Db 5 GK 6

RESULT 51

Q04131

ID Q04131 PRELIMINARY; PRT; 11 AA.  
AC Q04131;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Wound induced protein (Fragment).  
OS Lycopersicon esculentum (Tomato).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;  
OC lamiids; Solanales; Solanaceae; Solanum.  
OX NCBI\_TaxID=4081;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=pik-red; TISSUE=Pericarp;  
RX MEDLINE=91355936; PubMed=1715787;  
RA Parsons B.L., Mattoo A.K.;  
RT "Wound regulated accumulation of specific transcripts in tomato fruit:  
RT interactions with fruit development, ethylene and light.";  
RL Plant Mol. Biol. 17:453-464(1991).  
DR EMBL; X59884; CAA42539.1; -.  
DR PIR; S19775; S19775.  
FT NON\_TER 1 1  
SQ SEQUENCE 11 AA; 1278 MW; 92CB257828733325 CRC64;

Query Match 18.2%; Score 2; DB 10; Length 11;

Best Local Similarity 100.0%; Pred. No. 1e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KK 6  
||  
Db 5 KK 6

RESULT 52

P82336

ID P82336 PRELIMINARY; PRT; 11 AA.  
AC P82336;  
DT 01-JUN-2000 (TrEMBLrel. 14, Created)  
DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Unknown protein from 2D-page of thylakoid (SPOT125) (Fragment).  
OS Pisum sativum (Garden pea).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae; Pisum.  
OX NCBI\_TaxID=3888;  
RN [1]  
RP SEQUENCE, SUBCELLULAR LOCATION, AND DEVELOPMENTAL STAGE.

RC STRAIN=cv. DE GRACE; TISSUE=LEAF;  
 RX MEDLINE=20181728; PubMed=10715320;  
 RA Peltier J.-B., Friso G., Kalume D.E., Roepstorff P., Nilsson F.,  
 RA Adamska I., van Wijk K.J.;  
 RT "Proteomics of the chloroplast: systematic identification and  
 RT targeting analysis of lumenal and peripheral thylakoid proteins."  
 RL Plant Cell 12:319-341(2000).  
 CC -!- SUBCELLULAR LOCATION: CHLOROPLAST THYLAKOID MEMBRANE LUMEN OR  
 CC PERIPHERY.  
 CC -!- DEVELOPMENTAL STAGE: UNFOLDED AND FULLY DEVELOPED LEAVES.  
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
 CC PROTEIN IS: 5.8, ITS MW IS: 45.8 KDA.  
 DR GO; GO:0009507; C:chloroplast; IEA.  
 DR GO; GO:0009579; C:thylakoid; IEA.  
 KW Chloroplast; Thylakoid.  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1255 MW; 13511E6EDB1DDB10 CRC64;

Query Match 18.2%; Score 2; DB 10; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AE 2  
 ||  
 Db 2 AE 3

# RESULT 53

Q99N81

ID Q99N81 PRELIMINARY; PRT; 11 AA.  
 AC Q99N81;  
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
 DE Delta like 1 (Fragment).  
 GN DLL1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Nakayama K.;  
 RT "Multiple POU-binding motifs, recognized by tissue-specific nuclear  
 RT factor(S), are important for Dll1 gene expression in developing neural  
 RT precursor cells."  
 RL Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AB050457; BAB43867.1; -.  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1259 MW; 33C3634CBDC40B07 CRC64;

Query Match 18.2%; Score 2; DB 11; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 RA 11  
 ||

Db

6 RA 7

RESULT 54

Q9R1N6

ID Q9R1N6 PRELIMINARY; PRT; 11 AA.  
 AC Q9R1N6;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)  
 DE Glucosidase II alpha-subunit (Fragment).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99150222; PubMed=10024665;  
 RA Arendt C.W., Dawicki W., Ostergaard H.L.;  
 RT "Alternative splicing of transcripts encoding the alpha- and beta-  
 RT subunits of mouse glucosidase II in T lymphocytes."  
 RL Glycobiology 9:277-283(1999).  
 DR EMBL; AF066060; AAD43363.1; -.  
 DR EMBL; AF066059; AAD43363.1; JOINED.  
 FT NON\_TER 1 1  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1106 MW; 8EB4DA6C7DC1A455 CRC64;

Query Match 18.2%; Score 2; DB 11; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GK 5  
 ||  
 Db 8 GK 9

RESULT 55

Q9Z1H5

ID Q9Z1H5 PRELIMINARY; PRT; 11 AA.  
 AC Q9Z1H5;  
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)  
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Insulin receptor (Fragment).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=94365199; PubMed=8083370;  
 RA Huang Z., Bodkin N.L., Ortmeyer H.K., Hansen B.C., Shuldiner A.R.;  
 RT "Hyperinsulinemia is associated with altered insulin receptor mRNA  
 RT splicing in muscle of the spontaneously obese diabetic rhesus  
 RT monkey."  
 RL J. Clin. Invest. 94:1289-1296(1994).

RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Ying L.;  
 RL Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Liu Y.;  
 RL Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; L42997; AAC96365.1; -.  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 KW Receptor.  
 FT NON\_TER 1 1  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1052 MW; 9C25F7BAD8744865 CRC64;

Query Match 18.2%; Score 2; DB 11; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AE 2  
 ||  
 Db 8 AE 9

# RESULT 56

P81075

ID P81075 PRELIMINARY; PRT; 11 AA.  
 AC P81075; P97898; Q64728;  
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)  
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Major urinary protein 3 (MUP 3) (Fragment).  
 GN MUP1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J;  
 RX MEDLINE=88065510; PubMed=2824995;  
 RA Held W.A., Gallagher J.F., Hohman C.M., Kuhn N.J., Sampsell B.M.,  
 RA Hughes R.G. Jr.;  
 RT "Identification and characterization of functional genes encoding the  
 RT mouse major urinary proteins."  
 RL Mol. Cell. Biol. 7:3705-3712(1987).  
 CC -!- FUNCTION: BINDS PHEROMONES, THE PHEROMONES ARE RELEASED FROM  
 CC DRYING URINE OF MALES AND AFFECT THE SEXUAL BEHAVIOUR OF FEMALES.  
 CC -!- TISSUE SPECIFICITY: ABUNDANT IN THE URINE OF BOTH MALES AND  
 CC FEMALES. SYNTHESIZED IN THE LIVER AND MAMMARY GLAND.  
 CC -!- SIMILARITY: THIS PROTEIN BELONGS TO THE FAMILY OF SMALL  
 CC HYDROPHOBIC MOLECULE TRANSPORT PROTEINS.  
 DR EMBL; M17816; AAA40542.1; -.  
 DR EMBL; M17818; AAA40543.1; -.  
 DR PIR; I77447; I77447.  
 DR MGD; MGI:97233; Mup1.  
 DR GO; GO:0005550; F:pheromone binding; IEA.

DR GO; GO:0006810; P:transport; IEA.  
KW Pheromone-binding; Transport; Lipocalin; Multigene family.  
FT CONFLICT 4 4 MISSING (IN AAA40543).  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1248 MW; 5B16D68E27272727 CRC64;

Query Match 18.2%; Score 2; DB 11; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KM 9  
||  
Db 2 KM 3

#### RESULT 57

Q80WI3

ID Q80WI3 PRELIMINARY; PRT; 11 AA.  
AC Q80WI3;  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Somatostatin receptor subtype 4 (Fragment).  
GN RSSTR4.  
OS Rattus sp.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10118;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=95134278; PubMed=7832807;  
RA Xu Y., Bruno J.F., Berelowitz M.;  
RT "Characterization of the proximal promoter region of the rat  
RT somatostatin receptor gene, SSTR4."  
RL Biochem. Biophys. Res. Commun. 206:935-941(1995).  
DR EMBL; S75475; AAP31686.1; -.  
DR GO; GO:0004872; F:receptor activity; IEA.  
KW Receptor.  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1071 MW; 2820DE0E6731ADC7 CRC64;

Query Match 18.2%; Score 2; DB 11; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GG 4  
||  
Db 10 GG 11

#### RESULT 58

Q83083

ID Q83083 PRELIMINARY; PRT; 11 AA.  
AC Q83083;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

DE P13 mini peptide.  
 OS Leucania separata nuclear polyhedrosis virus (LsNPV).  
 OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;  
 OC Nucleopolyhedrovirus.  
 OX NCBI\_TaxID=41714;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96140622; PubMed=8572949;  
 RA Wang J.W., Qi Y.P., Huang Y.X., Li S.D.;  
 RT "Nucleotide sequence of a 1446 base pair Sall fragment and structure  
 RT of a novel early gene of Leucania seperata nuclear polyhedrosis  
 RT virus.";  
 RL Arch. Virol. 140:2283-2291(1995).  
 DR EMBL; U30303; AAA99737.1; -.  
 SQ SEQUENCE 11 AA; 1339 MW; F7BDBE0BD40DC401 CRC64;

Query Match 18.2%; Score 2; DB 12; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EG 3  
 ||  
 Db 10 EG 11

#### RESULT 59

Q9J1G3

ID Q9J1G3 PRELIMINARY; PRT; 11 AA.  
 AC Q9J1G3;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
 DE ORF2.  
 OS TT virus.  
 OC Viruses; ssDNA viruses; Circoviridae; Anellovirus.  
 OX NCBI\_TaxID=68887;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=TTV-SC314;  
 RX MEDLINE=20251008; PubMed=10790123;  
 RA Niel C., Saback F.L., Lampe E.;  
 RT "Coinfection with Multiple TT Virus Strains Belonging to Different  
 RT Genotypes Is a Common Event in Brazilian Healthy Adults.";  
 RL J. Clin. Microbiol. 38:1926-1930(2000).  
 DR EMBL; AF216458; AAF66894.1; -.  
 SQ SEQUENCE 11 AA; 1264 MW; D044FE23F771B5B9 CRC64;

Query Match 18.2%; Score 2; DB 12; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AE 2  
 ||  
 Db 2 AE 3

#### RESULT 60

O40974

ID O40974 PRELIMINARY; PRT; 11 AA.  
AC O40974;  
DT 01-JAN-1998 (TrEMBLrel. 05, Created)  
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Unidentified protein (Fragment).  
OS Cauliflower mosaic virus.  
OC Viruses; Retroid viruses; Caulimoviridae; Caulimovirus.  
OX NCBI\_TaxID=10641;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=90320145; PubMed=2371775;  
RA Vaden V.R., Melcher U.K.;  
RT "Recombination sites in Cauliflower mosaic virus DNAs: Implications  
RT for mechanisms of recombination.";  
RL Virology 177:717-726(1990).  
DR EMBL; M32808; AAA46361.1; -.  
FT NON\_TER 1 1  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1155 MW; 95F0E0D1DAA1E05A CRC64;

Query Match 18.2%; Score 2; DB 12; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GK 5  
||  
Db 10 GK 11

RESULT 61

Q8UUP1

ID Q8UUP1 PRELIMINARY; PRT; 11 AA.  
AC Q8UUP1;  
DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
DE Beta-TrCP protein (Fragment).  
GN BETA-TRCP.  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;  
OC Xenopodinae; Xenopus.  
OX NCBI\_TaxID=8355;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Carnevali F.;  
RL Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Ballarino M.;  
RT "Analisi strutturale e funzionale del gene beta-TrCP in Xenopus  
RT laevis.";  
RL Thesis (2001), Department of Genetica e Biologia Molecolare,  
RL University of Rome La Sapienza, Rome, Italy.  
DR EMBL; AJ428930; CAD21927.1; -.

FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1195 MW; CEB938EE35BEA5B9 CRC64;

Query Match 18.2%; Score 2; DB 13; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EG 3  
||  
Db 2 EG 3

RESULT 62

Q8JGW8

ID Q8JGW8 PRELIMINARY; PRT; 11 AA.  
AC Q8JGW8;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE Rhodopsin (Fragment).  
OS Ficedula albicollis.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Passeriformes; Muscicapidae; Ficedula.  
OX NCBI\_TaxID=59894;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C2B;  
RX MEDLINE=21918460; PubMed=11918793;  
RA Primmer C.R., Borge T., Lindell J., Saetre G.P.;  
RT "Single-nucleotide polymorphism characterization in species with  
RT limited available sequence information: high nucleotide diversity  
RT revealed in the avian genome.";  
RL Mol. Ecol. 11:603-612(2002).  
DR EMBL; AY069952; AAL50206.1; -.  
FT NON\_TER 1 1  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1226 MW; 7309D562D9C9C87B CRC64;

Query Match 18.2%; Score 2; DB 13; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EG 3  
||  
Db 4 EG 5

RESULT 63

Q90735

ID Q90735 PRELIMINARY; PRT; 11 AA.  
AC Q90735;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Beta-globin gene (Fragment).  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;



OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=81208060; PubMed=6263308;  
 RA Day L.E., Hirst A.J., Lai E.C., Mace M.Jr., Woo S.L.C.;  
 RT "5' domain and nucleotide sequence of an adult chicken chromosomal  
 RT beta-globin gene.";  
 RL Biochemistry 20:2091-2098(1981).  
 DR EMBL; V00378; CAA23677.1; -.  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1372 MW; 271C02021B1DC1B3 CRC64;

Query Match 18.2%; Score 2; DB 13; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AE 2  
 ||  
 Db 6 AE 7

#### RESULT 64

Q98YS3

ID Q98YS3 PRELIMINARY; PRT; 11 AA.  
 AC Q98YS3;  
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Truncated pol protein (Fragment).  
 GN POL.  
 OS Human immunodeficiency virus 1.  
 OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=985829;  
 RA Schmidt B., Walter H., Moschik G., Paatz C., Werwein M., Schwingel E.,  
 RA Korn K.;  
 RT "Recovery of HIV-1 pol gene sequences by direct sequencing of  
 RT amplification products derived from plasma samples.";  
 RL Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AF347394; AAK32471.1; -.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 11 AA; 1195 MW; E96941B8D878773A CRC64;

Query Match 18.2%; Score 2; DB 15; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GG 4  
 ||  
 Db 6 GG 7

#### RESULT 65

P88018

ID P88018 PRELIMINARY; PRT; 11 AA.  
AC P88018;  
DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE Envelope glycoprotein, C2-V5 region (Fragment).  
GN ENV.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=97138372; PubMed=8985398;  
RA Ganeshan S., Dickover R.E., Korber B.T., Bryson Y.J., Wolinsky S.M.;  
RT "Human immunodeficiency virus type 1 genetic evolution in children  
RT with different rates of development of disease.";  
RL J. Virol. 71:663-677(1997).  
DR EMBL; U48172; AAC56320.1; -.  
FT NON\_TER 1 1  
SQ SEQUENCE 11 AA; 1189 MW; 8E11B0D71B1DD735 CRC64;

Query Match 18.2%; Score 2; DB 15; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AE 2  
||  
Db 6 AE 7

RESULT 66

Q9AIY6

ID Q9AIY6 PRELIMINARY; PRT; 11 AA.  
AC Q9AIY6;  
DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Tryptophanyl-tRNA synthetase (Fragment).  
GN TRPS.  
OS Carsonella ruddii.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Candidatus Carsonella.  
OX NCBI\_TaxID=114186;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20336438; PubMed=10877784;  
RA Thao M.L., Moran N.A., Abbot P., Brennan E.B., Burckhardt D.H.,  
RA Baumann P.;  
RT "Cospeciation of psyllids and their primary prokaryotic  
RT endosymbionts.";  
RL Appl. Environ. Microbiol. 66:2898-2905(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21125546; PubMed=11222582;  
RA Clark M.A., Baumann L., Thao M.L., Moran N.A., Baumann P.;  
RT "Degenerative Minimalism in the Genome of a Psyllid Endosymbiont.";  
RL J. Bacteriol. 183:1853-1861(2001).

DR EMBL; AF211138; AAK15388.1; -.  
DR GO; GO:0004812; F:tRNA ligase activity; IEA.  
KW Aminoacyl-tRNA synthetase.  
FT NON\_TER 1 1  
SQ SEQUENCE 11 AA; 1295 MW; OCA993A5345B5720 CRC64;

Query Match 9.1%; Score 1; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 7.4e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 K 5  
|  
Db 8 K 8

#### RESULT 67

O68237

ID O68237 PRELIMINARY; PRT; 11 AA.  
AC O68237;  
DT 01-AUG-1998 (TrEMBLrel. 07, Created)  
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Plasmid cp32-4, possible partition proteins (Fragment).  
OS *Borrelia burgdorferi* (Lyme disease spirochete).  
OG Plasmid cp32-4.  
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; *Borrelia*.  
OX NCBI\_TaxID=139;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=B31;  
RX MEDLINE=98361033; PubMed=9695920;  
RA Stevenson B., Casjens S., Rosa P.;  
RT "Evidence of past recombination events among the genes encoding the  
RT Erp antigens of *Borrelia burgdorferi*."  
RL Microbiology 144:1869-1879(1998).  
DR EMBL; AF022481; AAC35449.1; -.  
DR GO; GO:0046821; C:extrachromosomal DNA; IEA.  
KW Plasmid.  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1237 MW; 50E3B714D45B5DD7 CRC64;

Query Match 9.1%; Score 1; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 7.4e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 M 9  
|  
Db 1 M 1

#### RESULT 68

Q48933

ID Q48933 PRELIMINARY; PRT; 11 AA.  
AC Q48933; P77701; Q48932;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)

DE Alkyl hydroperoxide reductase C (Fragment).  
 GN AHPC.  
 OS Mycobacterium bovis.  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
 OX NCBI\_TaxID=1765;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC35728, and ATCC35727;  
 RA Zhang Y., Deretic V.;  
 RL Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC35735;  
 RX MEDLINE=96256622; PubMed=8655566;  
 RA Dhandayuthapani S., Zhang Y., Deretic V.;  
 RT "Oxidative stress response and its role in sensitivity to isoniazid in  
 RT mycobacteria: characterization and inducibility of ahpc by peroxides in  
 RT Mycobacterium smegmatis and lack of expression in M. aurum and M.  
 RT tuberculosis.";  
 RL J. Bacteriol. 178:3641-3649(1996).  
 DR EMBL; U58031; AAB00320.1; -.  
 DR EMBL; U57979; AAA99830.1; -.  
 DR EMBL; U57978; AAA99829.1; -.  
 DR EMBL; U57762; AAB00317.1; -.  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1231 MW; 455099E3A87041A7 CRC64;

Query Match 9.1%; Score 1; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 7.4e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 G 3  
 |  
 Db 7 G 7

# RESULT 69

Q47451  
 ID Q47451 PRELIMINARY; PRT; 11 AA.  
 AC Q47451;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Plasmid pRJ1004 DNA (Fragment).  
 OS Escherichia coli.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Escherichia.  
 OX NCBI\_TaxID=562;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=pRJ1004;  
 RX MEDLINE=96130847; PubMed=8594334;  
 RA Brown N.L., Barrett S.R., Camakaris J., Lee B.T., Rouch D.A.;  
 RT "Molecular genetics and transport analysis of the copper-resistance  
 RT determinants (pco) from Escherichia coli plasmid pRJ1004.";  
 RL Mol. Microbiol. 17:1153-1166(1995).

DR EMBL; X83541; CAA58524.1; -.  
DR PIR; S70166; S52252.  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1195 MW; 47D864F8ADC1A057 CRC64;

Query Match 9.1%; Score 1; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 7.4e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 M 9  
|  
Db 1 M 1

RESULT 70

Q9AIZ7

ID Q9AIZ7 PRELIMINARY; PRT; 11 AA.  
AC Q9AIZ7;  
DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Tryptophanyl-tRNA synthetase (Fragment).  
GN TRPS.  
OS Carsonella ruddii.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Candidatus Carsonella.  
OX NCBI\_TaxID=114186;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20336438; PubMed=10877784;  
RA Thao M.L., Moran N.A., Abbot P., Brennan E.B., Burckhardt D.H.,  
RA Baumann P.;  
RT "Cospeciation of psyllids and their primary prokaryotic  
RT endosymbionts.";  
RL Appl. Environ. Microbiol. 66:2898-2905(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21125546; PubMed=11222582;  
RA Clark M.A., Baumann L., Thao M.L., Moran N.A., Baumann P.;  
RT "Degenerative Minimalism in the Genome of a Psyllid Endosymbiont.";  
RL J. Bacteriol. 183:1853-1861(2001).  
DR EMBL; AF211132; AAK15377.1; -.  
DR GO; GO:0004812; F:tRNA ligase activity; IEA.  
KW Aminoacyl-tRNA synthetase.  
FT NON\_TER 1 1  
SQ SEQUENCE 11 AA; 1333 MW; A28C67D6533059C6 CRC64;

Query Match 9.1%; Score 1; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 7.4e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 M 9  
|  
Db 4 M 4

RESULT 71

Q52526

ID Q52526 PRELIMINARY; PRT; 11 AA.  
AC Q52526;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Megaplasmid SYM nodulation node (Fragment).  
OS Rhizobium sp.  
OG Plasmid SYM.  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
OC Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.  
OX NCBI\_TaxID=391;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=41;  
RA Rostas K., Kondorosi E., Horvath B., Simoncsits A., Kondorosi A.;  
RT "Conservation of extended promoter regions of nodulation genes in  
RT Rhizobium.";  
RL Proc. Natl. Acad. Sci. U.S.A. 83:1757-1761(1986).  
DR EMBL; M13289; AAB86797.1; -.  
DR GO; GO:0046821; C:extrachromosomal DNA; IEA.  
KW Plasmid.  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1233 MW; C966816205BB1736 CRC64;

Query Match 9.1%; Score 1; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 7.4e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 E 2  
|  
Db 6 E 6

# RESULT 72

Q8KHL0

ID Q8KHL0 PRELIMINARY; PRT; 11 AA.  
AC Q8KHL0;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE Hypothetical protein (Fragment).  
OS Streptococcus gallolyticus.  
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;  
OC Streptococcus.  
OX NCBI\_TaxID=53354;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=4-C11, and 4-G10; TRANSPOSON=Tn5382-like;  
RA Dahl K.H., Sundsfjord A.;  
RT "vanB2 operons linked to Tn5382-like elements in Streptococcus strains  
RT from veal calves.";  
RL Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; AY035710; AAL07295.1; -.  
DR EMBL; AY035711; AAL07297.1; -.  
KW Hypothetical protein.  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1329 MW; 93207414D1EEAB5E CRC64;

Query Match 9.1%; Score 1; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 7.4e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 M 9  
|  
Db 1 M 1

RESULT 73

Q47602

ID Q47602 PRELIMINARY; PRT; 11 AA.  
AC Q47602;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE REase protein (Fragment).  
GN REASE.  
OS Escherichia coli.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Escherichia.  
OX NCBI\_TaxID=562;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=91139577; PubMed=1995588;  
RA Tao T., Bourne J.C., Blumenthal R.M.;  
RT "A family of regulatory genes associated with type II restriction-  
RT modification systems."  
RL J. Bacteriol. 173:1367-1375(1991).  
DR EMBL; M63620; AAA24558.1; -.  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1412 MW; 80ABB190C736DAAA CRC64;

Query Match 9.1%; Score 1; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 7.4e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 M 9  
|  
Db 1 M 1

RESULT 74

Q47606

ID Q47606 PRELIMINARY; PRT; 11 AA.  
AC Q47606;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE REase protein (Fragment).  
GN REASE.  
OS Escherichia coli.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Escherichia.  
OX NCBI\_TaxID=562;  
RN [1]

RP SEQUENCE FROM N.A.  
 RX MEDLINE=91139577; PubMed=1995588;  
 RA Tao T., Bourne J.C., Blumenthal R.M.;  
 RT "A family of regulatory genes associated with type II restriction-  
 RT modification systems.";  
 RL J. Bacteriol. 173:1367-1375(1991).  
 DR EMBL; M63622; AAA24562.1; -.  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1370 MW; 68C1FF9959CB133B CRC64;

Query Match 9.1%; Score 1; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 7.4e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 M 9  
 |  
 Db 1 M 1

# RESULT 75

Q8L2T4

ID Q8L2T4 PRELIMINARY; PRT; 11 AA.  
 AC Q8L2T4;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Histidinol phosphatase (Fragment).  
 OS Neisseria meningitidis.  
 OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;  
 OC Neisseriaceae; Neisseria.  
 OX NCBI\_TaxID=487;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=126E;  
 RX MEDLINE=22051050; PubMed=12055303;  
 RA Zhu P., Klutch M.J., Bash M.C., Tsang R.S.W., Ng L.K., Tsai C.M.;  
 RT "Genetic Diversity of Three Lgt Loci for Biosynthesis of  
 RT Lipooligosaccharide (LOS) in Neisseria Species.";  
 RL Microbiology 148:1833-1844(2002).  
 DR EMBL; AF470685; AAM33538.1; -.  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1273 MW; 01EC828D0AA72050 CRC64;

Query Match 9.1%; Score 1; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 7.4e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 M 9  
 |  
 Db 1 M 1

Search completed: April 8, 2004, 15:46:09  
 Job time : 28.7692 secs



OM protein - protein search, using sw model

Run on: April 8, 2004, 15:30:07 ; Search time 5.15385 Seconds  
(without alignments)  
111.135 Million cell updates/sec

Title: US-09-787-443A-19  
Perfect score: 11  
Sequence: 1 AEGGKKKKMRA 11

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 141681 seqs, 52070155 residues

Word size : 0

Total number of hits satisfying chosen parameters: 70

Minimum DB seq length: 11  
Maximum DB seq length: 11

Post-processing: Listing first 100 summaries

Database : SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result		%	Query				
No.	Score	Match	Length	DB	ID	Description	
1	3	27.3	11	1	PKC1_CARMO	P82684	carausius m
2	2	18.2	11	1	ASL2_BACSE	P83147	bacteroides
3	2	18.2	11	1	BPP4_BOTIN	P30424	bothrops in
4	2	18.2	11	1	CSI5_BACSU	P81095	bacillus su
5	2	18.2	11	1	ES1_RAT	P56571	rattus norv
6	2	18.2	11	1	FAR9_CALVO	P41864	calliphora
7	2	18.2	11	1	LADD_ONCMY	P81018	oncorhynchu
8	2	18.2	11	1	LSK1_LEUMA	P04428	leucophaea
9	2	18.2	11	1	LSKP_PERAM	P36885	periplaneta
10	2	18.2	11	1	MHBI_KLEPN	P80580	klebsiella
11	2	18.2	11	1	MORN_HUMAN	P01163	homo sapien
12	2	18.2	11	1	NUHM_CANFA	P49820	canis famil
13	2	18.2	11	1	PQQC_PSEFL	P55173	pseudomonas
14	2	18.2	11	1	PVK1_PERAM	P41837	periplaneta
15	2	18.2	11	1	Q2OA_COMTE	P80464	comamonas t
16	2	18.2	11	1	RRPL_CHAV	P13179	chandipura
17	2	18.2	11	1	RS30_ONCMY	P83328	oncorhynchu

18	1	9.1	11	1	ANGT_CRIGE	P09037	crinia geor
19	1	9.1	11	1	ASL1_BACSE	P83146	bacteroides
20	1	9.1	11	1	BPP3_BOTIN	P30423	bothrops in
21	1	9.1	11	1	BPPB_AGKHA	P01021	agkistrodon
22	1	9.1	11	1	BPP_AGKHP	P04562	agkistrodon
23	1	9.1	11	1	BRK_MEGFL	P12797	megascolia
24	1	9.1	11	1	CA21_LITCI	P82087	litoria cit
25	1	9.1	11	1	CA22_LITCI	P82088	litoria cit
26	1	9.1	11	1	CA31_LITCI	P82089	litoria cit
27	1	9.1	11	1	CA32_LITCI	P82090	litoria cit
28	1	9.1	11	1	CA41_LITCI	P82091	litoria cit
29	1	9.1	11	1	CA42_LITCI	P82092	litoria cit
30	1	9.1	11	1	CEP1_ACHFU	P22790	achatina fu
31	1	9.1	11	1	CORZ_PERAM	P11496	periplaneta
32	1	9.1	11	1	COXA_CANFA	P99501	canis famil
33	1	9.1	11	1	CX5A_CONAL	P58848	conus aulic
34	1	9.1	11	1	CX5B_CONAL	P58849	conus aulic
35	1	9.1	11	1	CXL1_CONMR	P58807	conus marmo
36	1	9.1	11	1	EFG_CLOPA	P81350	clostridium
37	1	9.1	11	1	FAR6_PENMO	P83321	penaeus mon
38	1	9.1	11	1	HS70_PINPS	P81672	pinus pinas
39	1	9.1	11	1	LPW_THETH	P05624	thermus the
40	1	9.1	11	1	MLG_THETS	P41989	theromyzon
41	1	9.1	11	1	NXSN_PSETE	P59072	pseudonaja
42	1	9.1	11	1	OAIF_SARBU	P83518	sarcophaga
43	1	9.1	11	1	RANC_RANPI	P08951	rana pipien
44	1	9.1	11	1	RE41_LITRU	P82074	litoria rub
45	1	9.1	11	1	RR2_CONAM	P42341	conopholis
46	1	9.1	11	1	T2P1_PROVU	P31031	proteus vul
47	1	9.1	11	1	TIN1_HOPTI	P82651	hoplobatrac
48	1	9.1	11	1	TIN4_HOPTI	P82654	hoplobatrac
49	1	9.1	11	1	TKC2_CALVO	P41518	calliphora
50	1	9.1	11	1	TKN1_PSEGU	P42986	pseudophryn
51	1	9.1	11	1	TKN1_UPEIN	P82026	uperoleia i
52	1	9.1	11	1	TKN1_UPERU	P08612	uperoleia r
53	1	9.1	11	1	TKN2_PSEGU	P42987	pseudophryn
54	1	9.1	11	1	TKN2_UPERU	P08616	uperoleia r
55	1	9.1	11	1	TKN3_PSEGU	P42988	pseudophryn
56	1	9.1	11	1	TKN4_PSEGU	P42989	pseudophryn
57	1	9.1	11	1	TKN5_PSEGU	P42990	pseudophryn
58	1	9.1	11	1	TKNA_CHICK	P19850	gallus gall
59	1	9.1	11	1	TKNA_GADMO	P28498	gadus morhu
60	1	9.1	11	1	TKNA_HORSE	P01290	equus cabal
61	1	9.1	11	1	TKNA_ONCMY	P28499	oncorhynchu
62	1	9.1	11	1	TKNA_RANCA	P22688	rana catesb
63	1	9.1	11	1	TKNA_RANRI	P29207	rana ridibu
64	1	9.1	11	1	TKNA_SCYCA	P41333	scyliorhinu
65	1	9.1	11	1	TKND_RANCA	P22691	rana catesb
66	1	9.1	11	1	TKN_ELEMO	P01293	eledone mos
67	1	9.1	11	1	TKN_PHYFU	P08615	physalaemus
68	1	9.1	11	1	UF05_MOUSE	P38643	mus musculu
69	1	9.1	11	1	ULAG_HUMAN	P31933	homo sapien
70	1	9.1	11	1	UXB2_YEAST	P99013	saccharomyc

# ALIGNMENTS

# RESULT 1

PKC1\_CARMO

ID PKC1\_CARMO STANDARD; PRT; 11 AA.  
AC P82684;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Pyrokinin-1 (Cam-PK-1) (FXPRL-Amide).  
OS Carausius morosus (Indian stick insect).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Orthopteroidea; Phasmatodea; Euphasmida; Phasmatoidea;  
OC Heteronemiidae; Carausius.  
OX NCBI\_TaxID=7022;  
RN [1]  
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.  
RC TISSUE=Corpora cardiaca;  
RA Predel R., Kellner R., Gaede G.;  
RT "Myotropic neuropeptides from the retrocerebral complex of the stick  
RT insect, Carausius morosus (Phasmatodea: Lonchodidae).";  
RL Eur. J. Entomol. 96:275-278(1999).  
CC -!- FUNCTION: Mediates visceral muscle contractile activity (myotropic  
CC activity).  
CC -!- MASS SPECTROMETRY: MW=1235; METHOD=MALDI.  
CC -!- SIMILARITY: Belongs to the pyrokinin family.  
DR InterPro; IPR001484; Pyrokinin.  
DR PROSITE; PS00539; PYROKININ; FALSE\_NEG.  
KW Neuropeptide; Amidation; Pyrokinin.  
FT MOD\_RES 11 11 AMIDATION.  
SQ SEQUENCE 11 AA; 1236 MW; 2BFA5225BB46C1A8 CRC64;

Query Match 27.3%; Score 3; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EGG 4  
|||  
Db 2 EGG 4

# RESULT 2

ASL2\_BACSE

ID ASL2\_BACSE STANDARD; PRT; 11 AA.  
AC P83147;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Acharan sulfate lyase 2 (EC 4.2.2.-) (Fragment).  
OS Bacteroides stercoris.  
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;  
OC Bacteroidaceae; Bacteroides.  
OX NCBI\_TaxID=46506;  
RN [1]  
RP SEQUENCE, FUNCTION, ENZYME REGULATION, AND SUBUNIT.  
RC STRAIN=HJ-15;  
RX MEDLINE=21223019; PubMed=11322884;  
RA Kim B.-T., Hong S.-W., Kim W.-S., Kim Y.S., Kim D.-H.;

RT "Purification and characterization of acharan sulfate lyases, two  
 RT novel heparinases, from Bacteroides stercoris HJ-15.";  
 RL Eur. J. Biochem. 268:2635-2641(2001).  
 CC -!- FUNCTION: Degrades acharan sulfate and, to a lesser extent,  
 CC heparin and heparan sulfate.  
 CC -!- ENZYME REGULATION: Inhibited by cupric ion, nitrogen and lead.  
 CC Activated by reducing agents, such as DL-dithiothreitol and 2-  
 CC mercaptoethanol.  
 CC -!- SUBUNIT: Monomer.  
 CC -!- PTM: The N-terminus is blocked.  
 CC -!- MISCELLANEOUS: Has an isoelectric point of 8.6. Its optimum pH is  
 CC 7.2 and optimum temperature 45 degrees Celsius.  
 KW Lyase; Heparin-binding.  
 FT NON\_TER 1 1  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1195 MW; D79D897C7AA451AD CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GG 4  
 ||  
 Db 8 GG 9

# RESULT 3

BPP4\_BOTIN  
 ID BPP4\_BOTIN STANDARD; PRT; 11 AA.  
 AC P30424;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Bradykinin-potentiating peptide S4,1,2 (Angiotensin-converting  
 DE enzyme inhibitor).  
 OS Bothrops insularis (Island jararaca) (Queimada jararaca).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
 OC Viperidae; Crotalinae; Bothrops.  
 OX NCBI\_TaxID=8723;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Venom;  
 RX MEDLINE=90351557; PubMed=2386615;  
 RA Cintra A.C.O., Vieira C.A., Giglio J.R.;  
 RT "Primary structure and biological activity of bradykinin potentiating  
 RT peptides from Bothrops insularis snake venom.";  
 RL J. Protein Chem. 9:221-227(1990).  
 CC -!- FUNCTION: This peptide both inhibits the activity of the  
 CC angiotensin-converting enzyme and enhances the action of  
 CC bradykinin by inhibiting the kinases that inactivate it.  
 CC It acts as an indirect hypotensive agent.  
 DR PIR; D37196; D37196.  
 KW Hypotensive agent; Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 SQ SEQUENCE 11 AA; 1143 MW; 20BBBF13C7741777 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.4e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GG 4  
||  
Db 2 GG 3

RESULT 4

CSI5\_BACSU  
ID CSI5\_BACSU STANDARD; PRT; 11 AA.  
AC P81095;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Cold shock protein CSI5 (11 kDa cold shock protein) (Fragment).  
OS Bacillus subtilis.  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
OX NCBI\_TaxID=1423;  
RN [1]  
RP SEQUENCE.  
RC STRAIN=168 / JH642;  
RA Graumann P.L., Schmid R., Marahiel M.A.;  
RL Submitted (OCT-1997) to Swiss-Prot.  
RN [2]  
RP CHARACTERIZATION.  
RC STRAIN=168 / JH642;  
RX MEDLINE=96345629; PubMed=8755892;  
RA Graumann P., Schroeder K., Schmid R., Marahiel M.A.;  
RT "Cold shock stress-induced proteins in Bacillus subtilis."  
RL J. Bacteriol. 178:4611-4619(1996).  
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.  
CC -!- INDUCTION: In response to low temperature.  
CC -!- CAUTION: Could not be found in the genome of B.subtilis 168.  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1360 MW; 15F6ECEE6322C330 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.4e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 MR 10  
||  
Db 1 MR 2

RESULT 5

ES1\_RAT  
ID ES1\_RAT STANDARD; PRT; 11 AA.  
AC P56571;  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE ES1 protein, mitochondrial (Fragment).  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=Wistar; TISSUE=Heart;  
 RA Li X.-P., Pleissner K.-P., Scheler C., Regitz-Zagrosek V., Salikov J.,  
 RA Jungblut P.R.;  
 RL Submitted (SEP-1998) to Swiss-Prot.  
 CC -!- SUBCELLULAR LOCATION: Mitochondrial (Potential).  
 CC -!- MISCELLANEOUS: By 2D-PAGE, the determined pI of this protein (spot  
 CC P2) is: 8.9, its MW is: 25 kDa.  
 CC -!- SIMILARITY: BELONGS TO THE ES1 FAMILY.  
 KW Mitochondrion.  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1142 MW; D862272D32C72DC2 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 RA 11  
 ||  
 Db 1 RA 2

#### RESULT 6

##### FAR9\_CALVO

ID FAR9\_CALVO STANDARD; PRT; 11 AA.  
 AC P41864;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE CalliFMRFamide 9.  
 OS Calliphora vomitoria (Blue blowfly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;  
 OC Calliphoridae; Calliphora.  
 OX NCBI\_TaxID=27454;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Thoracic ganglion;  
 RX MEDLINE=92196111; PubMed=1549595;  
 RA Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,  
 RA Rehfeld J.F., Thorpe A.;  
 RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2  
 RT neuropeptides (designated calliFMRFamides) from the blowfly  
 RT Calliphora vomitoria."  
 RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).  
 CC -!- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)  
 CC family.  
 DR PIR; I41978; I41978.  
 KW Neuropeptide; Amidation.  
 FT MOD\_RES 11 11 AMIDATION.  
 SQ SEQUENCE 11 AA; 1359 MW; 8160CE46CAA44321 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+04;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 MR 10  
||  
Db 9 MR 10

RESULT 7

LADD\_ONCMY

ID LADD\_ONCMY STANDARD; PRT; 11 AA.  
AC P81018;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE Ladderlectin (Fragment).  
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.  
OX NCBI\_TaxID=8022;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Blood;  
RX MEDLINE=97293418; PubMed=9149391;  
RA Jensen L.E., Thiel S., Petersen T.E., Jensenuis J.C.;  
RT "A rainbow trout lectin with multimeric structure."  
RL Comp. Biochem. Physiol. 116B:385-390(1997).  
CC -!- FUNCTION: Lectin that binds sepharose.  
CC -!- COFACTOR: Calcium is essential for sepharose binding.  
CC -!- SUBUNIT: Multimeric.  
KW Lectin; Calcium.  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1163 MW; 0B26227FF6D45404 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.4e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AE 2  
||  
Db 2 AE 3

RESULT 8

LSK1\_LEUMA

ID LSK1\_LEUMA STANDARD; PRT; 11 AA.  
AC P04428;  
DT 13-AUG-1987 (Rel. 05, Created)  
DT 13-AUG-1987 (Rel. 05, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Leucosulfakinin-I (LSK-I).  
OS Leucophaea maderae (Madeira cockroach).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;  
OC Blaberidae; Leucophaea.  
OX NCBI\_TaxID=6988;  
RN [1]

RP SEQUENCE.  
RX MEDLINE=86315858; PubMed=3749893;  
RA Nachman R.J., Holman G.M., Haddon W.F., Ling N.;  
RT "Leucosulfakinin, a sulfated insect neuropeptide with homology to  
RT gastrin and cholecystokinin.";  
RL Science 234:71-73(1986).  
CC -!- FUNCTION: Change the frequency and amplitude of contractions of  
CC the hingat. Inhibits muscle contraction of hindgut.  
CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.  
DR PIR; A01622; GMROL.  
DR InterPro; IPR001651; Gastrin.  
DR PROSITE; PS00259; GASTRIN; 1.  
KW Hormone; Amidation; Sulfation.  
FT MOD\_RES 6 6 SULFATION.  
FT MOD\_RES 11 11 AMIDATION.  
SQ SEQUENCE 11 AA; 1459 MW; 7E4E0680E86B5AAB CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.4e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 MR 10  
||  
Db 9 MR 10

#### RESULT 9

LSKP\_PERAM  
ID LSKP\_PERAM STANDARD; PRT; 11 AA.  
AC P36885;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 01-FEB-1996 (Rel. 33, Last annotation update)  
DE Perisulfakinin (Pea-SK-I).  
OS Periplaneta americana (American cockroach).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea;  
OC Blattidae; Periplaneta.  
OX NCBI\_TaxID=6978;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Corpora cardiaca;  
RX MEDLINE=90137190; PubMed=2615921;  
RA Veenstra J.A.;  
RT "Isolation and structure of two gastrin/CCK-like neuropeptides from  
RT the American cockroach homologous to the leucosulfakinins.";  
RL Neuropeptides 14:145-149(1989).  
CC -!- FUNCTION: Stimulates hindgut contractions.  
CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.  
DR PIR; A60656; A60656.  
DR InterPro; IPR001651; Gastrin.  
DR PROSITE; PS00259; GASTRIN; 1.  
KW Hormone; Amidation; Sulfation.  
FT MOD\_RES 6 6 SULFATION.  
FT MOD\_RES 11 11 AMIDATION.  
SQ SEQUENCE 11 AA; 1445 MW; 8B4E0680E86B5AAA CRC64;



Query Match 18.2%; Score 2; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.4e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 MR 10  
||  
Db 9 MR 10

RESULT 10

MHBI\_KLEPN

ID MHBI\_KLEPN STANDARD; PRT; 11 AA.  
AC P80580;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 01-NOV-1997 (Rel. 35, Last annotation update)  
DE Maleylpyruvate isomerase (EC 5.2.1.4) (Fragment).  
GN MHBI.  
OS Klebsiella pneumoniae.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Klebsiella.  
OX NCBI\_TaxID=573;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=96349117; PubMed=8760924;  
RA Robson N.D., Parrott S., Cooper R.A.;  
RT "In vitro formation of a catabolic plasmid carrying Klebsiella  
RT pneumoniae DNA that allows growth of Escherichia coli K-12 on 3-  
RT hydroxybenzoate.";  
RL Microbiology 142:2115-2120(1996).  
CC -!- CATALYTIC ACTIVITY: 3-maleylpyruvate = 3-fumarylpyruvate.  
KW Isomerase.  
FT NON TER 11 11  
SQ SEQUENCE 11 AA; 1387 MW; 1EE0E2DD49C9D5AB CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.4e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 RA 11  
||  
Db 10 RA 11

RESULT 11

MORN\_HUMAN

ID MORN\_HUMAN STANDARD; PRT; 11 AA.  
AC P01163;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Morphogenetic neuropeptide (Head activator) (HA).  
OS Homo sapiens (Human),  
OS Rattus norvegicus (Rat),  
OS Bos taurus (Bovine),  
OS Anthopleura elegantissima (Sea anemone), and  
OS Hydra attenuata (Hydra) (Hydra vulgaris).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606, 10116, 9913, 6110, 6087;  
 RN [1]  
 RP SEQUENCE.  
 RC SPECIES=Human, Rat, and Bovine;  
 RX MEDLINE=82035850; PubMed=7290191;  
 RA Bodenmuller H., Schaller H.C.;  
 RT "Conserved amino acid sequence of a neuropeptide, the head activator,  
 RT from coelenterates to humans."  
 RL Nature 293:579-580(1981).  
 RN [2]  
 RP SEQUENCE.  
 RC SPECIES=A.elegantissima, and H.attenuata;  
 RA Schaller H.C., Bodenmuller H.;  
 RT "Isolation and amino acid sequence of a morphogenetic peptide from  
 RT hydra."  
 RL Proc. Natl. Acad. Sci. U.S.A. 78:7000-7004(1981).  
 RN [3]  
 RP SYNTHESIS.  
 RX MEDLINE=82050803; PubMed=7297679;  
 RA Birr C., Zachmann B., Bodenmuller H., Schaller H.C.;  
 RT "Synthesis of a new neuropeptide, the head activator from hydra."  
 RL FEBS Lett. 131:317-321(1981).  
 RN [4]  
 RP FUNCTION.  
 RX MEDLINE=90059923; PubMed=2583101;  
 RA Schaller H.C., Druffel-Augustin S., Dubel S.;  
 RT "Head activator acts as an autocrine growth factor for NH15-CA2 cells  
 RT in the G2/mitosis transition."  
 RL EMBO J. 8:3311-3318(1989).  
 CC -!- FUNCTION: HA acts as an autocrine growth factor for neural cells  
 CC in the G2/mitosis transition.  
 CC -!- CAUTION: This peptide was first isolated from nerve cells of hydra  
 CC and was called head activator by the authors, because it induced  
 CC head-specific growth and differentiation in this animal. It has  
 CC been found in mammalian intestine and hypothalamus.  
 DR PIR; A01427; YHRT.  
 DR PIR; A93900; YHXA.E.  
 DR PIR; B01427; YHHU.  
 DR PIR; B93900; YHJFHY.  
 DR PIR; C01427; YHBO.  
 DR GK; P01163; -.  
 KW Growth factor; Cell cycle; Mitosis; Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 SQ SEQUENCE 11 AA; 1142 MW; 37927417C325B878 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GG 4  
 ||  
 Db 4 GG 5

NUHM\_CANFA  
 ID NUHM\_CANFA STANDARD; PRT; 11 AA.  
 AC P49820;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE NADH-ubiquinone oxidoreductase 24 kDa subunit (EC 1.6.5.3)  
 DE (EC 1.6.99.3) (Fragment).  
 GN NDUFV2.  
 OS Canis familiaris (Dog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 OX NCBI\_TaxID=9615;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Heart;  
 RX MEDLINE=98163340; PubMed=9504812;  
 RA Dunn M.J., Corbett J.M., Wheeler C.H.;  
 RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of  
 RT dog heart proteins.";  
 RL Electrophoresis 18:2795-2802(1997).  
 CC -!- FUNCTION: TRANSFER OF ELECTRONS FROM NADH TO THE RESPIRATORY  
 CC CHAIN. THE IMMEDIATE ELECTRON ACCEPTOR FOR THE ENZYME IS BELIEVED  
 CC TO BE UBIQUINONE. COMPONENT OF THE FLAVOPROTEIN-SULFUR (FP)  
 CC FRAGMENT OF THE ENZYME.  
 CC -!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.  
 CC -!- CATALYTIC ACTIVITY: NADH + acceptor = NAD(+) + reduced acceptor.  
 CC -!- COFACTOR: Binds 1 2Fe-2S cluster (Potential).  
 CC -!- SUBUNIT: Mammalian complex I is composed of 45 different subunits.  
 CC -!- SUBCELLULAR LOCATION: Matrix and cytoplasmic side of the  
 CC mitochondrial inner membrane.  
 CC -!- SIMILARITY: Belongs to the complex I 24 kDa subunit family.  
 DR HSC-2DPAGE; P49820; DOG.  
 DR InterPro; IPR002023; Cmplx1\_24kDa.  
 DR PROSITE; PS01099; COMPLEX1\_24K; PARTIAL.  
 KW Oxidoreductase; NAD; Ubiquinone; Mitochondrion; Metal-binding;  
 KW Iron-sulfur; Iron; 2Fe-2S.  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1099 MW; 267F5369C9C72DD8 CRC64;  
  
 Query Match 18.2%; Score 2; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 Qy 3 GG 4  
 ||  
 Db 3 GG 4

RESULT 13  
 PQQC\_PSEFL  
 ID PQQC\_PSEFL STANDARD; PRT; 11 AA.  
 AC P55173;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Coenzyme PQQ synthesis protein C (Pyrroloquinoline quinone

DE biosynthesis protein C) (Fragment).  
 GN PQQC.  
 OS Pseudomonas fluorescens.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
 OC Pseudomonadaceae; Pseudomonas.  
 OX NCBI\_TaxID=294;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CHA0;  
 RX MEDLINE=96064397; PubMed=8526497;  
 RA Schnider U., Keel C., Defago G., Haas D.;  
 RT "Tn5-directed cloning of pqq genes from Pseudomonas fluorescens CHA0:  
 RT mutational inactivation of the genes results in overproduction of the  
 RT antibiotic pyoluteorin.";  
 RL Appl. Environ. Microbiol. 61:3856-3864(1995).  
 CC -!- PATHWAY: Pyrroloquinoline quinone (PQQ) biosynthesis.  
 CC -!- SIMILARITY: Belongs to the pqqC family.  
 CC -----  
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 CC -----  
 DR EMBL; X87299; CAA60734.1; -.  
 DR PIR; S58244; S58244.  
 DR HAMAP; MF\_00654; -, 1.  
 KW PQQ biosynthesis.  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1182 MW; 89DF46E4C5B73771 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AE 2  
 ||  
 Db 9 AE 10

#### RESULT 14

##### PVK1\_PERAM

ID PVK1\_PERAM STANDARD; PRT; 11 AA.  
 AC P41837;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Periviscerokinin-1 (Pea-PVK-1).  
 OS Periplaneta americana (American cockroach).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea;  
 OC Blattidae; Periplaneta.  
 OX NCBI\_TaxID=6978;  
 RN [1]  
 RP SEQUENCE, AND SYNTHESIS.

RC TISSUE=Abdominal perisymphathetic organs;  
RX MEDLINE=95232021; PubMed=7716075;  
RA Predel R., Linde D., Rapus J., Vettermann S., Penzlin H.;  
RT "Periviscerokinin (Pea-PVK): a novel myotropic neuropeptide from the  
RT perisymphathetic organs of the American cockroach.";  
RL Peptides 16:61-66(1995).  
CC -!- FUNCTION: MYOACTIVE PEPTIDE; HAS EXCITORY ACTIONS ON THE  
CC HYPERNEURAL MUSCLE.  
KW Neuropeptide; Amidation.  
FT MOD\_RES 11 11 AMIDATION.  
SQ SEQUENCE 11 AA; 1114 MW; 39DB5419D7605728 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.4e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 MR 10  
||  
Db 9 MR 10

# RESULT 15

## Q20A\_COMTE

ID Q20A\_COMTE STANDARD; PRT; 11 AA.  
AC P80464;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Quinoline 2-oxidoreductase, alpha chain (EC 1.3.99.17) (Fragment).  
OS Comamonas testosteroni (Pseudomonas testosteroni).  
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;  
OC Comamonadaceae; Comamonas.  
OX NCBI\_TaxID=285;  
RN [1]  
RP SEQUENCE.  
RC STRAIN=63;  
RX MEDLINE=96035889; PubMed=7556204;  
RA Schach S., Tshisuaka B., Fetzner S., Lingens F.;  
RT "Quinoline 2-oxidoreductase and 2-oxo-1,2-dihydroquinoline 5,6-  
RT dioxygenase from Comamonas testosteroni 63. The first two enzymes in  
RT quinoline and 3-methylquinoline degradation.";  
RL Eur. J. Biochem. 232:536-544(1995).  
CC -!- FUNCTION: Converts (3-methyl-)-quinoline to (3-methyl-)2-oxo-  
CC 1,2-dihydroquinoline.  
CC -!- CATALYTIC ACTIVITY: Quinoline + acceptor + H(2)O = isoquinolin-  
CC 1(2H)-one + reduced acceptor.  
CC -!- COFACTOR: FAD, molybdenum and iron-sulfur.  
CC -!- PATHWAY: Degradation of quinoline and (3-methyl-)quinoline; first  
CC step.  
CC -!- SUBUNIT: Heterohexamer of two alpha chains, two beta chains, and  
CC two gamma chains (Probable).  
DR PIR; S66606; S66606.  
KW Oxidoreductase; Flavoprotein; FAD; Molybdenum.  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1213 MW; 869094322B1DC2CA CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;

Best Local Similarity 100.0%; Pred. No. 1.4e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AE 2  
||  
Db 6 AE 7

RESULT 16

RRPL\_CHAV

ID RRPL\_CHAV STANDARD; PRT; 11 AA.  
AC P13179;  
DT 01-JAN-1990 (Rel. 13, Created)  
DT 01-JAN-1990 (Rel. 13, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE RNA polymerase beta subunit (EC 2.7.7.48) (Large structural protein)  
DE (L protein) (Fragment).  
GN L.  
OS Chandipura virus (strain I653514).  
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
OC Rhabdoviridae; Vesiculovirus.  
OX NCBI\_TaxID=11273;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=89299473; PubMed=2741347;  
RA Masters P.S., Bhella R.S., Butcher M., Patel B., Ghosh H.P.,  
RA Banerjee A.K.;  
RT "Structure and expression of the glycoprotein gene of Chandipura  
RT virus."  
RL Virology 171:285-290(1989).  
CC -!- FUNCTION: THIS PROTEIN IS PROBABLY A COMPONENT OF THE ACTIVE  
CC POLYMERASE. IT MAY FUNCTION IN RNA SYNTHESIS, CAPPING, AS WELL AS  
CC METHYLATION OF CAPS, AND POLY(A) SYNTHESIS.  
CC -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +  
CC {RNA} (N).  
CC -!- SUBUNIT: THOUGHT TO FORM A TRANSCRIPTION COMPLEX WITH THE  
CC NUCLEOCAPSID (N) PROTEIN.  
CC -!- SIMILARITY: WITH THE L PROTEIN OF OTHER RHABDOVIRUSES AND  
CC PARAMYXOVIRUSES.  
CC -----  
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CC -----  
DR EMBL; J04350; AAA42917.1; -.  
KW Transferase; RNA-directed RNA polymerase.  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1189 MW; 0335D6E3AAB2D764 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.4e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AE 2  
||  
Db 10 AE 11

RESULT 17

RS30\_ONCMY

ID RS30\_ONCMY STANDARD; PRT; 11 AA.  
AC P83328;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE 40S ribosomal protein S30 (Fragment).  
GN FAU.  
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.  
OX NCBI\_TaxID=8022;  
RN [1]  
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.  
RC TISSUE=Skin mucus;  
RX MEDLINE=22142142; PubMed=12147245;  
RA Fernandes J.M.O., Smith V.J.;  
RT "A novel antimicrobial function for a ribosomal peptide from rainbow  
RT trout skin.";  
RL Biochem. Biophys. Res. Commun. 296:167-171(2002).  
CC -!- FUNCTION: Has antibacterial activity against Gram-positive  
CC bacteria.  
CC -!- MASS SPECTROMETRY: MW=6676.6; METHOD=MALDI.  
CC -!- SIMILARITY: Belongs to the S30E family of ribosomal proteins.  
KW Ribosomal protein; Antibiotic.  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1123 MW; 2312AB630DD735B8 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.4e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GK 5  
||  
Db 10 GK 11

RESULT 18

ANGT\_CRIGE

ID ANGT\_CRIGE STANDARD; PRT; 11 AA.  
AC P09037;  
DT 01-NOV-1988 (Rel. 09, Created)  
DT 01-NOV-1988 (Rel. 09, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Crinia-angiotensin II.  
OS Crinia georgiana (Quacking frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;  
OC Myobatrachinae; Crinia.  
OX NCBI\_TaxID=8374;

RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Skin secretion;  
 RX MEDLINE=80024575; PubMed=488254;  
 RA Erspamer V., Melchiorri P., Nakajima T., Yasuhara T., Endean R.;  
 RT "Amino acid composition and sequence of crinia-angiotensin, an  
 RT angiotensin II-like endecapeptide from the skin of the Australian  
 RT frog *Crinia georgiana*.";  
 RL Experientia 35:1132-1133(1979).  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Skin.  
 DR PIR; S07207; S07207.  
 KW Vasoconstrictor.  
 SQ SEQUENCE 11 AA; 1271 MW; 8A0921F7DB50440A CRC64;  
  
 Query Match 9.1%; Score 1; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 9.4e+04;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1  
 |  
 Db 1 A 1

# RESULT 19

## ASL1\_BACSE

ID ASL1\_BACSE STANDARD; PRT; 11 AA.  
 AC P83146;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Acharan sulfate lyase 1 (EC 4.2.2.-) (Fragment).  
 OS Bacteroides stercoris.  
 OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;  
 OC Bacteroidaceae; Bacteroides.  
 OX NCBI\_TaxID=46506;  
 RN [1]  
 RP SEQUENCE, FUNCTION, ENZYME REGULATION, AND SUBUNIT.  
 RC STRAIN=HJ-15;  
 RX MEDLINE=21223019; PubMed=11322884;  
 RA Kim B.-T., Hong S.-W., Kim W.-S., Kim Y.S., Kim D.-H.;  
 RT "Purification and characterization of acharan sulfate lyases, two  
 RT novel heparinases, from *Bacteroides stercoris* HJ-15.";  
 RL Eur. J. Biochem. 268:2635-2641(2001).  
 CC -!- FUNCTION: Degrades acharan sulfate and, to a lesser extent,  
 CC heparin and heparan sulfate.  
 CC -!- ENZYME REGULATION: Inhibited by cupric ion, nitrogen and cobalt.  
 CC Activated by reducing agents, such as DL-dithiothreitol and 2-  
 CC mercaptoethanol.  
 CC -!- SUBUNIT: Monomer.  
 CC -!- PTM: The N-terminus is blocked.  
 CC -!- MISCELLANEOUS: Has an isoelectric point of 8.6. Its optimum pH is  
 CC 7.2 and optimum temperature 45 degrees Celsius.  
 KW Lyase; Heparin-binding.  
 FT NON\_TER 1 1  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1395 MW; 01B2DAA241E865AB CRC64;



Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.4e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 G 3  
|  
Db 6 G 6

RESULT 20

BPP3\_BOTIN

ID BPP3\_BOTIN STANDARD; PRT; 11 AA.  
AC P30423;  
DT 01-APR-1993 (Rel. 25, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Bradykinin-potentiating peptide S4,3,2 (10C) (Angiotensin-converting  
DE enzyme inhibitor).  
OS Bothrops insularis (Island jararaca) (Queimada jararaca).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
OC Viperidae; Crotalinae; Bothrops.  
OX NCBI\_TaxID=8723;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Venom;  
RX MEDLINE=90351557; PubMed=2386615;  
RA Cintra A.C.O., Vieira C.A., Giglio J.R.;  
RT "Primary structure and biological activity of bradykinin potentiating  
RT peptides from Bothrops insularis snake venom.";  
RL J. Protein Chem. 9:221-227(1990).  
CC -!- FUNCTION: This peptide both inhibits the activity of the  
CC angiotensin-converting enzyme and enhances the action of  
CC bradykinin by inhibiting the kinases that inactivate it.  
CC It acts as an indirect hypotensive agent.  
DR PIR; C37196; C37196.  
KW Hypotensive agent; Pyrrolidone carboxylic acid.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
SQ SEQUENCE 11 AA; 1199 MW; 20B25813C7741777 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.4e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 G 3  
|  
Db 3 G 3

RESULT 21

BPPB\_AGKHA

ID BPPB\_AGKHA STANDARD; PRT; 11 AA.  
AC P01021;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Bradykinin-potentiating peptide B (Angiotensin-converting  
DE enzyme inhibitor).  
OS Agkistrodon halys blomhoffii (Mamushi) (Gloydus blomhoffii).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
OC Viperidae; Crotalinae; Gloydus.  
OX NCBI\_TaxID=242054;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Venom;  
RA Kato H., Suzuki T.;  
RT "Amino acid sequence of bradykinin-potentiating peptide isolated from  
RT the venom of Agkistrodon halys blomhoffii.";  
RL Proc. Jpn. Acad., B, Phys. Biol. Sci. 46:176-181(1970).  
CC -!- FUNCTION: This peptide both inhibits the activity of the  
CC angiotensin-converting enzyme and enhances the action of  
CC bradykinin by inhibiting the kinases that inactivate it.  
CC It acts as an indirect hypotensive agent.  
DR PIR; A01254; XASNBA.  
KW Hypotensive agent; Pyrrolidone carboxylic acid.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
SQ SEQUENCE 11 AA; 1199 MW; 295CBF0627741777 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.4e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 G 3  
|  
Db 2 G 2

# RESULT 22

BPP\_AGKHP  
ID BPP\_AGKHP STANDARD; PRT; 11 AA.  
AC P04562;  
DT 13-AUG-1987 (Rel. 05, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Bradykinin-potentiating peptide (Angiotensin-converting  
DE enzyme inhibitor).  
OS Agkistrodon halys pallas (Chinese water mocassin) (Gloydus halys  
OS pallas).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
OC Viperidae; Crotalinae; Gloydus.  
OX NCBI\_TaxID=8714;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Venom;  
RX MEDLINE=86177022; PubMed=3008123;  
RA Chi C.-W., Wang S.-Z., Xu L.-G., Wang M.-Y., Lo S.-S., Huang W.-D.;  
RT "Structure-function studies on the bradykinin potentiating peptide  
RT from Chinese snake venom (Agkistrodon halys pallas).";  
RL Peptides 6 Suppl. 3:339-342(1985).  
CC -!- FUNCTION: This peptide both inhibits the activity of the  
CC angiotensin-converting enzyme and enhances the action of

CC bradykinin by inhibiting the kinases that inactivate it.  
 CC It acts as an indirect hypotensive agent.  
 DR PIR; JC0002; XAVIBH.  
 KW Hypotensive agent; Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 SQ SEQUENCE 11 AA; 1112 MW; 30BABF1277686777 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 9.4e+04;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 G 3  
 |  
 Db 2 G 2

# RESULT 23

## BRK\_MEGFL

ID BRK\_MEGFL STANDARD; PRT; 11 AA.  
 AC P12797;  
 DT 01-OCT-1989 (Rel. 12, Created)  
 DT 01-OCT-1989 (Rel. 12, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Megascoliakinin ([Thr6]bradykinin-Lys-Ala) [Contains: Bradykinin-like peptide ([Thr6]bradykinin)].  
 OS Megascolia flavifrons (Garden dagger wasp) (Solitary wasp).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;  
 OC Scoliidae; Megascolia.  
 OX NCBI\_TaxID=7437;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Venom;  
 RX MEDLINE=87293024; PubMed=3617088;  
 RA Yasuhara T., Mantel P., Nakajima T., Piek T.;  
 RT "Two kinins isolated from an extract of the venom reservoirs of the  
 RT solitary wasp Megascolia flavifrons."  
 RL Toxicon 25:527-535(1987).  
 RN [2]  
 RP SEQUENCE.  
 RC TISSUE=Venom;  
 RA Nakajima T., Piek T., Yashuara T., Mantel P.;  
 RT "Two kinins isolated from the venom of Megascolia flavifrons."  
 RL Toxicon 26:34-34(1988).  
 CC -!- FUNCTION: Both proteins have bradykinin-like, although lower  
 CC activities (e.g. smooth muscle contraction).  
 CC -!- SUBCELLULAR LOCATION: Secreted; wasp venom reservoirs.  
 CC -!- SIMILARITY: Belongs to the bradykinin family.  
 DR PIR; B26744; B26744.  
 DR GO; GO:0005615; C:extracellular space; IDA.  
 DR GO; GO:0045776; P:negative regulation of blood pressure; ISS.  
 DR GO; GO:0045987; P:positive regulation of smooth muscle contra. . .; TAS.  
 KW Bradykinin; Vasodilator.  
 FT PEPTIDE 1 11 MEGASCOLIAKININ.  
 FT PEPTIDE 1 9 BRADYKININ-LIKE PEPTIDE.  
 SQ SEQUENCE 11 AA; 1273 MW; 33867393D771A9C8 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.4e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 R 10  
|  
Db 1 R 1

RESULT 24

CA21\_LITCI

ID CA21\_LITCI STANDARD; PRT; 11 AA.

AC P82087;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Caerulein 2.1/2.1Y4.

OS Litoria citropa (Australian blue mountains tree frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;

OC Pelodyadinae; Litoria.

OX NCBI\_TaxID=94770;

RN [1]

RP SEQUENCE, AND MASS SPECTROMETRY.

RC TISSUE=Skin secretion;

RX MEDLINE=20057701; PubMed=10589099;

RA Wabnitz P.A., Bowie J.H., Tyler M.J.;

RT "Caerulein-like peptides from the skin glands of the Australian blue

RT mountains tree frog Litoria citropa. Part 1. Sequence determination

RT using electrospray mass spectrometry.";

RL Rapid Commun. Mass Spectrom. 13:2498-2502(1999).

CC -!- FUNCTION: Hypotensive neuropeptide (Probable).

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- TISSUE SPECIFICITY: Skin dorsal glands.

CC -!- PTM: Isoform 2.1Y4 differs from isoform 2.1 in not being

CC sulfated.

CC -!- MASS SPECTROMETRY: MW=1372; METHOD=Electrospray.

CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.

DR InterPro; IPR001651; Gastrin.

DR PROSITE; PS00259; GASTRIN; FALSE\_NEG.

KW Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;

KW Pyrrolidone carboxylic acid.

FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.

FT MOD\_RES 4 4 SULFATION.

FT MOD\_RES 11 11 AMIDATION.

SQ SEQUENCE 11 AA; 1312 MW; 10DAB7C4EDD861BB CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.4e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 G 3  
|  
Db 6 G 6

RESULT 25

## CA22\_LITCI

ID CA22\_LITCI STANDARD; PRT; 11 AA.  
AC P82088;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Caerulein 2.2/2.2Y4.  
OS Litoria citropa (Australian blue mountains tree frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;  
OC Pelodyadinae; Litoria.  
OX NCBI\_TaxID=94770;  
RN [1]  
RP SEQUENCE, AND MASS SPECTROMETRY.  
RC TISSUE=Skin secretion;  
RX MEDLINE=20057701; PubMed=10589099;  
RA Wabnitz P.A., Bowie J.H., Tyler M.J.;  
RT "Caerulein-like peptides from the skin glands of the Australian blue  
RT mountains tree frog Litoria citropa. Part 1. Sequence determination  
RT using electrospray mass spectrometry."  
RL Rapid Commun. Mass Spectrom. 13:2498-2502(1999).  
CC -!- FUNCTION: Hypotensive neuropeptide (Probable).  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Skin dorsal glands.  
CC -!- PTM: Isoform 2.2Y4 differs from isoform 2.2 in not being  
CC sulfated.  
CC -!- MASS SPECTROMETRY: MW=1388; METHOD=Electrospray.  
CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.  
DR InterPro; IPR001651; Gastrin.  
DR PROSITE; PS00259; GASTRIN; FALSE\_NEG.  
KW Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;  
KW Pyrrolidone carboxylic acid.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
FT MOD\_RES 4 4 SULFATION.  
FT MOD\_RES 11 11 AMIDATION.  
SQ SEQUENCE 11 AA; 1328 MW; 10DAB894EDD861BB CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.4e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 G 3  
|  
Db 6 G 6

## RESULT 26

## CA31\_LITCI

ID CA31\_LITCI STANDARD; PRT; 11 AA.  
AC P82089;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Caerulein 3.1/3.1Y4.  
OS Litoria citropa (Australian blue mountains tree frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;

OC Pelodryadinae; Litoria.  
 OX NCBI\_TaxID=94770;  
 RN [1]  
 RP SEQUENCE, AND MASS SPECTROMETRY.  
 RC TISSUE=Skin secretion;  
 RX MEDLINE=20057701; PubMed=10589099;  
 RA Wabnitz P.A., Bowie J.H., Tyler M.J.;  
 RT "Caerulein-like peptides from the skin glands of the Australian blue  
 RT mountains tree frog Litoria citropa. Part 1. Sequence determination  
 RT using electrospray mass spectrometry."  
 RL Rapid Commun. Mass Spectrom. 13:2498-2502(1999).  
 CC -!- FUNCTION: Hypotensive neuropeptide (Probable).  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Skin dorsal glands.  
 CC -!- PTM: Isoform 3.1Y4 differs from isoform 3.1 in not being  
 CC sulfated.  
 CC -!- MASS SPECTROMETRY: MW=1407; METHOD=Electrospray.  
 CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.  
 DR InterPro; IPR001651; Gastrin.  
 DR PROSITE; PS00259; GASTRIN; FALSE\_NEG.  
 KW Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;  
 KW Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 4 4 SULFATION.  
 FT MOD\_RES 11 11 AMIDATION.  
 SQ SEQUENCE 11 AA; 1347 MW; 10DAB7D67861A86B CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 9.4e+04;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 G 3  
 |  
 Db 5 G 5

# RESULT 27

CA32\_LITCI

ID CA32\_LITCI STANDARD; PRT; 11 AA.  
 AC P82090;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Caerulein 3.2/3.2Y4.  
 OS Litoria citropa (Australian blue mountains tree frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;  
 OC Pelodryadinae; Litoria.  
 OX NCBI\_TaxID=94770;  
 RN [1]  
 RP SEQUENCE, AND MASS SPECTROMETRY.  
 RC TISSUE=Skin secretion;  
 RX MEDLINE=20057701; PubMed=10589099;  
 RA Wabnitz P.A., Bowie J.H., Tyler M.J.;  
 RT "Caerulein-like peptides from the skin glands of the Australian blue  
 RT mountains tree frog Litoria citropa. Part 1. Sequence determination  
 RT using electrospray mass spectrometry."

RL Rapid Commun. Mass Spectrom. 13:2498-2502(1999).  
 CC -!- FUNCTION: Hypotensive neuropeptide (Probable).  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Skin dorsal glands.  
 CC -!- PTM: Isoform 3.2Y4 differs from isoform 3.2 in not being  
 CC sulfated.  
 CC -!- MASS SPECTROMETRY: MW=1423; METHOD=Electrospray.  
 CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.  
 DR InterPro; IPR001651; Gastrin.  
 DR PROSITE; PS00259; GASTRIN; FALSE\_NEG.  
 KW Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;  
 KW Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 4 4 SULFATION.  
 FT MOD\_RES 11 11 AMIDATION.  
 SQ SEQUENCE 11 AA; 1363 MW; 10DAB8867861A86B CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 9.4e+04;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 G 3  
 |  
 Db 5 G 5

# RESULT 28

## CA41\_LITCI

ID CA41\_LITCI STANDARD; PRT; 11 AA.  
 AC P82091;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Caerulein 4.1/4.1Y4.  
 OS Litoria citropa (Australian blue mountains tree frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;  
 OC Pelodryadinae; Litoria.  
 OX NCBI\_TaxID=94770;  
 RN [1]  
 RP SEQUENCE, AND MASS SPECTROMETRY.  
 RC TISSUE=Skin secretion;  
 RX MEDLINE=20057701; PubMed=10589099;  
 RA Wabnitz P.A., Bowie J.H., Tyler M.J.;  
 RT "Caerulein-like peptides from the skin glands of the Australian blue  
 RT mountains tree frog Litoria citropa. Part 1. Sequence determination  
 RT using electrospray mass spectrometry."  
 RL Rapid Commun. Mass Spectrom. 13:2498-2502(1999).  
 CC -!- FUNCTION: Hypotensive neuropeptide (Probable).  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Skin dorsal glands.  
 CC -!- PTM: Isoform 4.1Y4 differs from isoform 4.1 in not being  
 CC sulfated.  
 CC -!- MASS SPECTROMETRY: MW=1388; METHOD=Electrospray.  
 CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.  
 DR InterPro; IPR001651; Gastrin.  
 DR PROSITE; PS00259; GASTRIN; FALSE\_NEG.

KW Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;  
 KW Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 4 4 SULFATION.  
 FT MOD\_RES 11 11 AMIDATION.  
 SQ SEQUENCE 11 AA; 1328 MW; 10DAB7C4F5B861BB CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 9.4e+04;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 G 3  
 |  
 Db 6 G 6

# RESULT 29

## CA42\_LITCI

ID CA42\_LITCI STANDARD; PRT; 11 AA.  
 AC P82092;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Caerulein 4.2/4.2Y4.  
 OS Litoria citropa (Australian blue mountains tree frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;  
 OC Pelodyadinae; Litoria.  
 OX NCBI\_TaxID=94770;  
 RN [1]  
 RP SEQUENCE, AND MASS SPECTROMETRY.  
 RC TISSUE=Skin secretion;  
 RX MEDLINE=20057701; PubMed=10589099;  
 RA Wabnitz P.A., Bowie J.H., Tyler M.J.;  
 RT "Caerulein-like peptides from the skin glands of the Australian blue  
 RT mountains tree frog Litoria citropa. Part 1. Sequence determination  
 RT using electrospray mass spectrometry."  
 RL Rapid Commun. Mass Spectrom. 13:2498-2502(1999).  
 CC -!- FUNCTION: Hypotensive neuropeptide (Probable).  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Skin dorsal glands.  
 CC -!- PTM: Isoform 4.2Y4 differs from isoform 4.2 in not being  
 CC sulfated.  
 CC -!- MASS SPECTROMETRY: MW=1404; METHOD=Electrospray.  
 CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.  
 DR InterPro; IPR001651; Gastrin.  
 DR PROSITE; PS00259; GASTRIN; FALSE\_NEG.  
 KW Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;  
 KW Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 4 4 SULFATION.  
 FT MOD\_RES 11 11 AMIDATION.  
 SQ SEQUENCE 11 AA; 1344 MW; 10DAB894F5B861BB CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 9.4e+04;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



Qy 3 G 3  
|  
Db 6 G 6

RESULT 30

CEP1\_ACHFU

ID CEP1\_ACHFU STANDARD; PRT; 11 AA.  
AC P22790;  
DT 01-AUG-1991 (Rel. 19, Created)  
DT 01-AUG-1991 (Rel. 19, Last sequence update)  
DT 01-DEC-1992 (Rel. 24, Last annotation update)  
DE Cardio-excitatory peptide-1 (ACEP-1).  
OS Achatina fulica (Giant African snail).  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;  
OC Sigmurethra; Achatinoidea; Achatinidae; Achatina.  
OX NCBI\_TaxID=6530;  
RN [1]  
RP SEQUENCE.  
RC STRAIN=Ferussac; TISSUE=Heart atrium;  
RX MEDLINE=90211261; PubMed=2322251;  
RA Fujimoto K., Ohta N., Yoshida M., Kubota I., Muneoka Y., Kobayashi M.;  
RT "A novel cardio-excitatory peptide isolated from the atria of the  
RT African giant snail, Achatina fulica.";  
RL Biochem. Biophys. Res. Commun. 167:777-783(1990).  
CC -!- FUNCTION: Potentiates the beat of the ventricle, and has also  
CC excitatory actions on the penis retractor muscle, the buccal  
CC muscle and the identified neurons controlling the buccal muscle  
CC movement of achatina.  
CC -!- SIMILARITY: TO POSSIBLE PEPTIDE L5 FROM APLYSIA.  
DR PIR; A34662; A34662.  
KW Hormone; Amidation.  
FT MOD RES 11 11 AMIDATION.  
SQ SEQUENCE 11 AA; 1305 MW; 82D6D5B9C7741365 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.4e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 G 3  
|  
Db 2 G 2

RESULT 31

CORZ\_PERAM

ID CORZ\_PERAM STANDARD; PRT; 11 AA.  
AC P11496;  
DT 01-OCT-1989 (Rel. 12, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Corazonin.  
OS Periplaneta americana (American cockroach).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea;  
OC Blattidae; Periplaneta.

OX NCBI\_TaxID=6978;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Corpora cardiaca;  
 RX MEDLINE=89325572; PubMed=2753132;  
 RA Veenstra J.A.;  
 RT "Isolation and structure of corazonin, a cardioactive peptide from  
 RT the American cockroach.";  
 RL FEBS Lett. 250:231-234(1989).  
 CC -!- FUNCTION: Cardioactive peptide. Corazonin is probably involved  
 CC in the physiological regulation of the heart beat.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 DR PIR; S05002; S05002.  
 KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 11 11 AMIDATION.  
 SQ SEQUENCE 11 AA; 1387 MW; C7CFF32D6415AB46 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 9.4e+04;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 G 3  
 |  
 Db 8 G 8

# RESULT 32

COXA\_CANFA  
 ID COXA\_CANFA STANDARD; PRT; 11 AA.  
 AC P99501;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Cytochrome c oxidase polypeptide Va (EC 1.9.3.1) (Fragment).  
 GN COX5A.  
 OS Canis familiaris (Dog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 OX NCBI\_TaxID=9615;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Heart;  
 RX MEDLINE=98163340; PubMed=9504812;  
 RA Dunn M.J., Corbett J.M., Wheeler C.H.;  
 RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of  
 RT dog heart proteins.";  
 RL Electrophoresis 18:2795-2802(1997).  
 CC -!- FUNCTION: This is the heme A-containing chain of cytochrome c  
 CC oxidase, the terminal oxidase in mitochondrial electron transport.  
 CC -!- CATALYTIC ACTIVITY: 4 ferrocycytochrome c + O(2) = 4 ferricytochrome  
 CC c + 2 H(2)O.  
 CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.  
 CC -!- SIMILARITY: Belongs to the cytochrome c oxidase Va family.  
 DR HSC-2DPAGE; P99501; DOG.  
 DR InterPro; IPR003204; Cyt\_c\_ox5A.  
 DR Pfam; PF02284; COX5A; 1.

KW Oxidoreductase; Heme; Mitochondrion; Inner membrane.  
FT NON TER 11 11  
SQ SEQUENCE 11 AA; 1274 MW; 910B35C5B1AB11F5 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.4e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 G 3  
|  
Db 3 G 3

RESULT 33

CX5A\_CONAL

ID CX5A\_CONAL STANDARD; PRT; 11 AA.

AC P58848;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Conotoxin au5a.

OS Conus aulicus (Court cone).

OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;

OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;

OC Neogastropoda; Conoidea; Conidae; Conus.

OX NCBI\_TaxID=89437;

RN [1]

RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.

RC TISSUE=Venom;

RX MEDLINE=99452958; PubMed=10521453;

RA Walker C.S., Steel D., Jacobsen R.B., Lirazan M.B., Cruz L.J.,

RA Hooper D., Shetty R., DelaCruz R.C., Nielsen J.S., Zhou L.M.,

RA Bandyopadhyay P., Craig A.G., Olivera B.M.;

RT "The T-superfamily of conotoxins.";

RL J. Biol. Chem. 274:30664-30671(1999).

RN [2]

RP ERRATUM.

RA Walker C.S., Steel D., Jacobsen R.B., Lirazan M.B., Cruz L.J.,

RA Hooper D., Shetty R., DelaCruz R.C., Nielsen J.S., Zhou L.M.,

RA Bandyopadhyay P., Craig A.G., Olivera B.M.;

RL J. Biol. Chem. 274:36030-36030(1999).

CC -!- FUNCTION: Causes dorsal fins drooping in fish. No effect is  
observed when injected into mice.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.

CC -!- MASS SPECTROMETRY: MW=1436.6; METHOD=LSIMS.

CC -!- SIMILARITY: Belongs to the conotoxin T-superfamily.

DR PIR; A59146; A59146.

KW Toxin.

FT DISULFID 2 9

FT DISULFID 3 10

SQ SEQUENCE 11 AA; 1441 MW; 21A36775440059D7 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.4e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 R 10  
|  
Db 7 R 7

RESULT 34

CX5B\_CONAL

ID CX5B\_CONAL STANDARD; PRT; 11 AA.  
AC P58849;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Conotoxin au5b.  
OS Conus aulicus (Court cone).  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;  
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;  
OC Neogastropoda; Conoidea; Conidae; Conus.  
OX NCBI\_TaxID=89437;  
RN [1]  
RP SEQUENCE, AND MASS SPECTROMETRY.  
RC TISSUE=Venom;  
RX MEDLINE=99452958; PubMed=10521453;  
RA Walker C.S., Steel D., Jacobsen R.B., Lirazan M.B., Cruz I.J.,  
RA Hooper D., Shetty R., Delacruz R.C., Nielsen J.S., Zhou L.M.,  
RA Bandyopadhyay P., Craig A.G., Olivera B.M.;  
RT "The T-superfamily of conotoxins."  
RL J. Biol. Chem. 274:30664-30671(1999).  
RN [2]  
RP ERRATUM.  
RA Walker C.S., Steel D., Jacobsen R.B., Lirazan M.B., Cruz I.J.,  
RA Hooper D., Shetty R., Delacruz R.C., Nielsen J.S., Zhou L.M.,  
RA Bandyopadhyay P., Craig A.G., Olivera B.M.;  
RL J. Biol. Chem. 274:36030-36030(1999).  
CC -!- FUNCTION: Causes dorsal fins drooping in fish. No effect is  
CC observed when injected into mice (By similarity).  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.  
CC -!- MASS SPECTROMETRY: MW=1388.6; METHOD=LSIMS.  
CC -!- SIMILARITY: Belongs to the conotoxin T-superfamily.  
DR PIR; B59146; B59146.  
KW Toxin.  
FT DISULFID 2 9  
FT DISULFID 3 10  
SQ SEQUENCE 11 AA; 1393 MW; 21A36775440042D7 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.4e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 R 10  
|  
Db 7 R 7

RESULT 35

CXL1\_CONMR

ID CXL1\_CONMR STANDARD; PRT; 11 AA.

AC P58807;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Lambda-conotoxin CMrVIA.  
 OS Conus marmoreus (Marble cone).  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;  
 OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;  
 OC Neogastropoda; Conoidea; Conidae; Conus.  
 OX NCBI\_TaxID=42752;  
 RN [1]  
 RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.  
 RC TISSUE=Venom;  
 RX MEDLINE=20564325; PubMed=10988292;  
 RA Balaji R.A., Ohtake A., Sato K., Gopalakrishnakone P., Kini R.M.,  
 RA Seow K.T., Bay B.-H.;  
 RT "Lambda-conotoxins, a new family of conotoxins with unique disulfide  
 RT pattern and protein folding. Isolation and characterization from the  
 RT venom of Conus marmoreus.";  
 RL J. Biol. Chem. 275:39516-39522(2000).  
 CC -!- FUNCTION: Inhibits the neuronal noradrenaline transporter.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.  
 CC -!- MASS SPECTROMETRY: MW=1237.93; MW\_ERR=0.21; METHOD=Electrospray.  
 CC -!- SIMILARITY: Belongs to the chi/lambda-conotoxin family.  
 KW Neurotoxin; Toxin; Hydroxylation.  
 FT DISULFID 2 11  
 FT DISULFID 3 8  
 FT MOD\_RES 10 10 HYDROXYLATION.  
 SQ SEQUENCE 11 AA; 1226 MW; 277AAC60B7232B58 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 9.4e+04;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 G 3  
 |  
 Db 4 G 4

#### RESULT 36

EFG\_CLOPA  
 ID EFG\_CLOPA STANDARD; PRT; 11 AA.  
 AC P81350;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Elongation factor G (EF-G) (CP 5) (Fragment).  
 GN FUSA.  
 OS Clostridium pasteurianum.  
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;  
 OC Clostridium.  
 OX NCBI\_TaxID=1501;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=W5;  
 RX MEDLINE=98291870; PubMed=9629918;

RA Flengsrud R., Skjeldal L.;  
 RT "Two-dimensional gel electrophoresis separation and N-terminal  
 RT sequence analysis of proteins from Clostridium pasteurianum W5."  
 RL Electrophoresis 19:802-806(1998).  
 CC -!- FUNCTION: This protein promotes the GTP-dependent translocation of  
 CC the nascent protein chain from the A-site to the P-site of the  
 CC ribosome.  
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -!- SIMILARITY: Belongs to the GTP-binding elongation factor family.  
 CC EF-G/EF-2 subfamily.  
 DR InterPro; IPR000795; EF\_GTPbind.  
 DR PROSITE; PS00301; EFAC\_TOR\_GTP; PARTIAL.  
 KW Elongation factor; Protein biosynthesis; GTP-binding.  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1337 MW; 412E71F1D9C33B17 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 9.4e+04;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 K 5  
 |  
 Db 1 K 1

#### RESULT 37

FAR6\_PENMO  
 ID FAR6\_PENMO STANDARD; PRT; 11 AA.  
 AC P83321;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE FMRFamide-like neuropeptide FLP6 (DGRTPALRLRF-amide).  
 OS Penaeus monodon (Penaeid shrimp).  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;  
 OC Penaeidae; Penaeus.  
 OX NCBI\_TaxID=6687;  
 RN [1]  
 RP SEQUENCE, AND MASS SPECTROMETRY.  
 RC TISSUE=Eyestalk;  
 RX MEDLINE=21956277; PubMed=11959015;  
 RA Sithigorngul P., Pupuem J., Krungkasem C., Longyant S.,  
 RA Chaivisuthangkura P., Sithigorngul W., Petsom A.;  
 RT "Seven novel FMRFamide-like neuropeptide sequences from the eyestalk  
 RT of the giant tiger prawn Penaeus monodon."  
 RL Comp. Biochem. Physiol. 131B:325-337(2002).  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- MASS SPECTROMETRY: MW=1301.8; METHOD=MALDI.  
 CC -!- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)  
 CC family.  
 DR GO; GO:0007218; P:neuropeptide signaling pathway; TAS.  
 KW Neuropeptide; Amidation.  
 FT MOD\_RES 11 11 AMIDATION.  
 SQ SEQUENCE 11 AA; 1301 MW; 9A19C860072DC771 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;

Best Local Similarity 100.0%; Pred. No. 9.4e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 G 3  
|  
Db 2 G 2

RESULT 38

HS70\_PINPS

ID HS70\_PINPS STANDARD; PRT; 11 AA.  
AC P81672;  
DT 15-JUL-1999 (Rel. 38, Created)  
DT 15-JUL-1999 (Rel. 38, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Heat shock 70 kDa protein (Fragment).  
OS Pinus pinaster (Maritime pine).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.  
OX NCBI\_TaxID=71647;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Needle;  
RX MEDLINE=99274088; PubMed=10344291;  
RA Costa P., Pionneau C., Bauw G., Dubos C., Bahrman N., Kremer A.,  
RA Frigerio J.-M., Plomion C.;  
RT "Separation and characterization of needle and xylem maritime pine  
RT proteins.";  
RL Electrophoresis 20:1098-1108(1999).  
CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this protein  
CC (spot N164) is: 5.4, its MW is: 73 kDa.  
CC -!- SIMILARITY: Belongs to the heat shock protein 70 family.  
KW ATP-binding; Heat shock; Multigene family.  
FT NON\_TER 1 1  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1228 MW; 037C1BE8DAA44DD0 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.4e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 E 2  
|  
Db 2 E 2

RESULT 39

LPW\_THETH

ID LPW\_THETH STANDARD; PRT; 11 AA.  
AC P05624;  
DT 01-NOV-1988 (Rel. 09, Created)  
DT 01-NOV-1988 (Rel. 09, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE Trp operon leader peptide.  
GN TRPL.  
OS Thermus thermophilus.  
OC Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;

OC Thermus.  
 OX NCBI\_TaxID=274;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=HB8 / ATCC 27634;  
 RX MEDLINE=89000781; PubMed=2844259;  
 RA Sato S., Nakada Y., Kanaya S., Tanaka T.;  
 RT "Molecular cloning and nucleotide sequence of *Thermus thermophilus*  
 RT HB8 trpE and trpG."  
 RL Biochim. Biophys. Acta 950:303-312(1988).  
 CC -!- FUNCTION: THIS PROTEIN IS INVOLVED IN CONTROL OF THE BIOSYNTHESIS  
 CC OF TRYPTOPHAN.

CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----

DR EMBL; X07744; CAA30565.1; -.  
 KW Tryptophan biosynthesis; Leader peptide.  
 SQ SEQUENCE 11 AA; 1228 MW; 364B295A772DC5A7 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 9.4e+04;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 M 9  
 |  
 Db 1 M 1

#### RESULT 40

##### MLG\_THETS

ID MLG\_THETS STANDARD; PRT; 11 AA.  
 AC P41989;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Melanotropin gamma (Gamma-melanocyte stimulating hormone) (Gamma-MSH).  
 OS *Theromyzon tessulatum* (Leech).  
 OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;  
 OC Rhynchobdellida; Glossiphoniidae; *Theromyzon*.  
 OX NCBI\_TaxID=13286;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Brain;  
 RX MEDLINE=94298944; PubMed=8026574;  
 RA Salzet M., Wattez C., Bulet P., Malecha J.;  
 RT "Isolation and structural characterization of a novel peptide related  
 RT to gamma-melanocyte stimulating hormone from the brain of the leech  
 RT *Theromyzon tessulatum*."  
 RL FEBS Lett. 348:102-106(1994).  
 CC -!- SIMILARITY: Belongs to the POMC family.  
 DR PIR; S45698; S45698.



KW Hormone; Amidation.  
FT MOD RES 11 11 AMIDATION.  
SQ SEQUENCE 11 AA; 1486 MW; 2DB8FACE6409C1E8 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.4e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 M 9  
|  
Db 3 M 3

RESULT 41

NXSN\_PSETE

ID NXSN\_PSETE STANDARD; PRT; 11 AA.  
AC P59072;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Short neurotoxin N1 (Alpha neurotoxin) (Fragment).  
OS Pseudonaja textilis (Eastern brown snake).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
OC Elapidae; Acanthophiinae; Pseudonaja.  
OX NCBI\_TaxID=8673;  
RN [1]  
RP SEQUENCE, AND MASS SPECTROMETRY.  
RC TISSUE=Venom;  
RX MEDLINE=99449602; PubMed=10518793;  
RA Gong N.L., Armugam A., Jeyaseelan K.;  
RT "Postsynaptic short-chain neurotoxins from Pseudonaja textilis: cDNA  
RT cloning, expression and protein characterization.";  
RL Eur. J. Biochem. 265:982-989(1999).  
CC -!- FUNCTION: Lethal neurotoxin, binds and inhibits nicotinic  
CC acetylcholine receptors (nAChR).  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.  
CC -!- MASS SPECTROMETRY: MW=6236; METHOD=Electrospray.  
CC -!- MISCELLANEOUS: LD(50) is 0.84 mg/kg by intravenous injection.  
CC -!- SIMILARITY: Belongs to the snake toxin family.  
DR InterPro; IPR003571; Snake\_toxin.  
DR PROSITE; PS00272; SNAKE\_TOXIN; PARTIAL.  
KW Toxin; Neurotoxin; Postsynaptic neurotoxin;  
KW Acetylcholine receptor inhibitor; Multigene family.  
FT UNSURE 3 3  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1319 MW; 0D1EF0C81B58732B CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.4e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 K 5  
|  
Db 5 K 5

# RESULT 42

OAIF\_SARBU

ID OAIF\_SARBU STANDARD; PRT; 11 AA.  
AC P83518;  
DT 10-OCT-2003 (Rel. 42, Created)  
DT 10-OCT-2003 (Rel. 42, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Ovary-derived ACE interactive factor (Neb-ODAIF) [Contains: Neb-ODAIF(1-9); Neb-ODAIF(1-7)].  
OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;  
OC Sarcophagidae; Sarcophaga.  
OX NCBI\_TaxID=7385;  
RN [1]  
RP SEQUENCE, SYNTHESIS, CHARACTERIZATION, AND MASS SPECTROMETRY.  
RC TISSUE=Ovary;  
RX MEDLINE=22272747; PubMed=12383874;  
RA Vandingenen A., Hens K., Baggerman G., Macours N., Schoofs L.,  
RA De Loof A., Huybrechts R.;  
RT "Isolation and characterization of an angiotensin converting enzyme  
RT substrate from vitellogenic ovaries of Neobellieria bullata.";  
RL Peptides 23:1853-1863(2002).  
CC -!- FUNCTION: Substrate for angiotensin converting enzyme (ACE) in  
CC vitro.  
CC -!- PTM: ACE hydrolyzes Neb-ODAIF by sequentially cleaving off two C-  
CC terminal dipeptides.  
CC -!- MASS SPECTROMETRY: MW=1312.7; METHOD=MALDI; RANGE=1-11.  
CC -!- SIMILARITY: To the N-terminal part of insect vitellogenins.  
FT PEPTIDE 1 11 NEB-ODAIF.  
FT PEPTIDE 1 9 NEB-ODAIF(1-9).  
FT PEPTIDE 1 7 NEB-ODAIF(1-7).  
SQ SEQUENCE 11 AA; 1314 MW; 4E114BB566C5A763 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.4e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 K 5  
|  
Db 2 K 2

# RESULT 43

RANC\_RANPI

ID RANC\_RANPI STANDARD; PRT; 11 AA.  
AC P08951;  
DT 01-NOV-1988 (Rel. 09, Created)  
DT 01-NOV-1988 (Rel. 09, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Ranatensin-C.  
OS Rana pipiens (Northern leopard frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.  
OX NCBI\_TaxID=8404;  
RN [1]

RP SEQUENCE.  
 RC TISSUE=Skin secretion;  
 RX MEDLINE=84131098; PubMed=6141890;  
 RA Nakajima T.;  
 RL Unpublished results, cited by:  
 RL Erspamer V., Erspamer G.F., Mazzanti G., Endean R.;  
 RL Comp. Biochem. Physiol. 77C:99-108(1984).  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Skin.  
 CC -!- SIMILARITY: Belongs to the bombesin/neuromedin B/ranatensin family.  
 DR InterPro; IPR000874; Bombesin.  
 DR Pfam; PF02044; Bombesin; 1.  
 DR PROSITE; PS00257; BOMBESIN; 1.  
 KW Amphibian defense peptide; Bombesin family; Amidation.  
 FT MOD RES 11 11 AMIDATION.  
 SQ SEQUENCE 11 AA; 1304 MW; D6C9885A61ADC366 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 9.4e+04;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1  
 |  
 Db 6 A 6

#### RESULT 44

RE41\_LITRU  
 ID RE41\_LITRU STANDARD; PRT; 11 AA.  
 AC P82074;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Rubellidin 4.1.  
 OS Litoria rubella (Desert tree frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;  
 OC Pelodyadinae; Litoria.  
 OX NCBI\_TaxID=104895;  
 RN [1]  
 RP SEQUENCE, AND MASS SPECTROMETRY.  
 RC TISSUE=Skin secretion;  
 RA Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,  
 RA Tyler M.J., Wallace J.C.;  
 RT "The structure of new peptides from the Australin red tree frog  
 RT 'Litoria rubella'. The skin peptide profile as a probe for the study  
 RT of evolutionary trends of amphibians."  
 RL Aust. J. Chem. 49:955-963(1996).  
 CC -!- FUNCTION: Shows neither neuropeptide activity nor antibiotic activity.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.  
 CC -!- MASS SPECTROMETRY: MW=1039; METHOD=FAB.  
 KW Amphibian defense peptide; Amidation.  
 FT MOD RES 11 11 AMIDATION.  
 SQ SEQUENCE 11 AA; 1040 MW; 84ED5CBC2877205A CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 9.4e+04;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 G 3  
 |  
 Db 1 G 1

RESULT 45

RR2\_CONAM

ID RR2\_CONAM STANDARD; PRT; 11 AA.

AC P42341;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Chloroplast 30S ribosomal protein S2 (Fragment).

GN RPS2.

OS Conopholis americana (Squawroot).

OG Chloroplast.

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;

OC lamids; Lamiales; Orobanchaceae; Orobancheae; Conopholis.

OX NCBI\_TaxID=4179;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=92145776; PubMed=1723664;

RA Taylor G., Wolfe K.H., Morden C.W., Depamphilis C.W., Palmer J.D.;

RT "Lack of a functional plastid tRNA(Cys) gene is associated with loss  
 of photosynthesis in a lineage of parasitic plants.";

RL Curr. Genet. 20:515-518(1991).

CC -!- SIMILARITY: Belongs to the S2P family of ribosomal proteins.

CC

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DR EMBL; X64567; CAA45868.1; -.

DR PIR; S32575; S32575.

DR HAMAP; MF\_00291; -; 1.

DR InterPro; IPR001865; Ribosomal\_S2.

DR PROSITE; PS00962; RIBOSOMAL\_S2\_1; PARTIAL.

DR PROSITE; PS00963; RIBOSOMAL\_S2\_2; PARTIAL.

KW Ribosomal protein; Chloroplast.

FT NON\_TER 11 11

SQ SEQUENCE 11 AA; 1497 MW; 76CD719954536B44 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;

Best Local Similarity 100.0%; Pred. No. 9.4e+04;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 E 2

Db 11 E 11

RESULT 46

T2P1\_PROVU

ID T2P1\_PROVU STANDARD; PRT; 11 AA.  
AC P31031;  
DT 01-JUL-1993 (Rel. 26, Created)  
DT 01-JUL-1993 (Rel. 26, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Type II restriction enzyme PvuI (EC 3.1.21.4) (Endonuclease PvuI)  
DE (R.PvuI) (Fragment).  
GN PVUIR.  
OS Proteus vulgaris.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Proteus.  
OX NCBI\_TaxID=585;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ATCC 13315;  
RX MEDLINE=93087186; PubMed=1454536;  
RA Smith M.D., Longo M., Gerard G.F., Chatterjee D.K.;  
RT "Cloning and characterization of genes for the PvuI restriction and  
RT modification system."  
RL Nucleic Acids Res. 20:5743-5747(1992).  
CC -!- FUNCTION: RECOGNIZES THE DOUBLE-STRANDED SEQUENCE CGATCG AND  
CC CLEAVES AFTER T-4.  
CC -!- CATALYTIC ACTIVITY: Endonucleolytic cleavage of DNA to give  
CC specific double-stranded fragments with terminal 5'-phosphates.  
CC -----  
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CC -----  
DR EMBL; L04163; AAA25660.1; -.  
DR PIR; S35490; S35490.  
DR REBASE; 1541; PvuI.  
KW Restriction system; Hydrolase; Nuclease; Endonuclease.  
FT NON\_TER 1 1  
SQ SEQUENCE 11 AA; 1300 MW; 9F0CDE7955B72B1A CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.4e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 E 2  
|  
Db 5 E 5

RESULT 47

TIN1\_HOPTI

ID TIN1\_HOPTI STANDARD; PRT; 11 AA.  
AC P82651;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Tigerinin-1.  
OS Hoplobatrachus tigerinus (Indian bull frog) (Rana tigerina).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae;  
OC Hoplobatrachus.  
OX NCBI\_TaxID=103373;  
RN [1]  
RP SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND DISULFIDE BONDS.  
RC TISSUE=Skin secretion;  
RX PubMed=11031261;  
RA Purna Sai K., Jaganadham M.V., Vairamani M., Raju N.P.,  
RA Devi A.S., Nagaraj R., Sitaram N.;  
RT "Tigerinins: novel antimicrobial peptides from the Indian frog Rana  
RT tigerina.";  
RL J. Biol. Chem. 276:2701-2707(2001).  
CC -!- FUNCTION: Antibacterial activity against B.subtilis, E.coli,  
CC S.aureus, M.luteus, P.putida and S.cerevisiae.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Skin.  
CC -!- MASS SPECTROMETRY: MW=1342; METHOD=MALDI.  
KW Amphibian defense peptide; Antibiotic; Fungicide; Amidation.  
FT DISULFID 2 10  
FT MOD\_RES 11 11 AMIDATION.  
SQ SEQUENCE 11 AA; 1344 MW; A2087DC960476056 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.4e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 M 9  
|  
Db 4 M 4

#### RESULT 48

TIN4\_HOPTI  
ID TIN4\_HOPTI STANDARD; PRT; 11 AA.  
AC P82654;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Tigerinin-4.  
OS Hoplobatrachus tigerinus (Indian bull frog) (Rana tigerina).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae;  
OC Hoplobatrachus.  
OX NCBI\_TaxID=103373;  
RN [1]  
RP SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND DISULFIDE BONDS.  
RC TISSUE=Skin secretion;  
RX PubMed=11031261;  
RA Purna Sai K., Jaganadham M.V., Vairamani M., Raju N.P.,

RA Devi A.S., Nagaraj R., Sitaram N.;  
 RT "Tigerinins: novel antimicrobial peptides from the Indian frog Rana  
 RT tigerina.";  
 RL J. Biol. Chem. 276:2701-2707(2001).  
 CC -!- FUNCTION: Antibacterial activity against B.subtilis, E.coli,  
 CC S.aureus, M.luteus, P.putida and S.cerevisiae.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Skin.  
 CC -!- MASS SPECTROMETRY: MW=1247; METHOD=MALDI.  
 KW Amphibian defense peptide; Antibiotic.  
 FT DISULFID 3 11  
 SQ SEQUENCE 11 AA; 1248 MW; 117D8EFD37605DCB CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 9.4e+04;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 R 10  
 |  
 Db 1 R 1

#### RESULT 49

TKC2\_CALVO  
 ID TKC2\_CALVO STANDARD; PRT; 11 AA.  
 AC P41518;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Callitachykinin II.  
 OS Calliphora vomitoria (Blue blowfly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;  
 OC Calliphoridae; Calliphora.  
 OX NCBI\_TaxID=27454;  
 RN [1]  
 RP SEQUENCE, AND SYNTHESIS.  
 RX MEDLINE=95075727; PubMed=7984492;  
 RA Lundquist C.T., Clottens F.L., Holman G.M., Nichols R., Nachman R.J.,  
 RA Naessel D.R.;  
 RT "Callitachykinin I and II, two novel myotropic peptides isolated from  
 RT the blowfly, Calliphora vomitoria, that have resemblances to  
 RT tachykinins.";  
 RL Peptides 15:761-768(1994).  
 CC -!- FUNCTION: Myoactive peptide.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: SOME SIMILARITY TO TACHYKININS.  
 KW Tachykinin; Neuropeptide; Amidation.  
 FT MOD\_RES 11 11 AMIDATION.  
 SQ SEQUENCE 11 AA; 1103 MW; 15D7E3F9C9CDD444 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 9.4e+04;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 G 3  
 |

Db 1 G 1

RESULT 50

TKN1\_PSEGU

ID TKN1\_PSEGU STANDARD; PRT; 11 AA.  
AC P42986;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Kassinin-like peptide K-I (PG-KI).  
OS Pseudophryne guentheri (Guenther's toadlet).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;  
OC Myobatrachinae; Pseudophryne.  
OX NCBI\_TaxID=30349;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Skin secretion;  
RX MEDLINE=90287814; PubMed=2356157;  
RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,  
RA Roberts J.D., Melchiorri P., Erspamer V.;  
RT "Six novel tachykinin- and bombesin-related peptides from the skin of  
RT the Australian frog Pseudophryne guntheri.";  
RL Peptides 11:299-304(1990).  
CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,  
CC evoke behavioral responses, are potent vasodilators and  
CC secretagogues, and contract (directly or indirectly) many smooth  
CC muscles.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Skin.  
CC -!- SIMILARITY: Belongs to the tachykinin family.  
DR PIR; B60409; B60409.  
DR InterPro; IPR002040; Tachy\_Neurokinin.  
DR InterPro; IPR008215; Tachykinin.  
DR Pfam; PF02202; Tachykinin; 1.  
DR SMART; SM00203; TK; 1.  
DR PROSITE; PS00267; TACHYKININ; 1.  
KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;  
KW Pyrrolidone carboxylic acid.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
FT MOD\_RES 11 11 AMIDATION.  
SQ SEQUENCE 11 AA; 1269 MW; 3DBA7C37C9CB1AB7 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.4e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 E 2  
|  
Db 6 E 6

RESULT 51

TKN1\_UPEIN

ID TKN1\_UPEIN STANDARD; PRT; 11 AA.  
AC P82026;



DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Uperin 1.1.  
 OS Uperoleia inundata (Floodplain toadlet).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;  
 OC Myobatrachinae; Uperoleia.  
 OX NCBI\_TaxID=104953;  
 RN [1]  
 RP SEQUENCE, AND MASS SPECTROMETRY.  
 RC TISSUE=Skin secretion;  
 RA Bradford A.M., Raftery M.J., Bowie J.H., Tyler M.J., Wallace J.C.,  
 RA Adams G.W., Severini C.;  
 RT "Novel uperin peptides from the dorsal glands of the australian  
 RT floodplain toadlet Uperoleia inundata.";  
 RL Aust. J. Chem. 49:475-484(1996).  
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,  
 CC evoke behavioral responses, are potent vasodilators and  
 CC secretagogues, and contract (directly or indirectly) many smooth  
 CC muscles.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Skin dorsal glands.  
 CC -!- MASS SPECTROMETRY: MW=1208; METHOD=FAB.  
 CC -!- SIMILARITY: Belongs to the tachykinin family.  
 DR InterPro; IPR002040; Tachy\_Neurokinin.  
 DR Pfam; PF02202; Tachykinin; 1.  
 DR PROSITE; PS00267; TACHYKININ; 1.  
 KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;  
 KW Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 11 11 AMIDATION.  
 SQ SEQUENCE 11 AA; 1226 MW; 3293693E59CDD457 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 9.4e+04;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1  
 |  
 Db 2 A 2

# RESULT 52

## TKN1\_UPERU

ID TKN1\_UPERU STANDARD; PRT; 11 AA.  
 AC P08612;  
 DT 01-AUG-1988 (Rel. 08, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Uperolein.  
 OS Uperoleia rugosa (Wrinkled toadlet).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;  
 OC Myobatrachinae; Uperoleia.  
 OX NCBI\_TaxID=8368;  
 RN [1]

RP SEQUENCE.  
RC TISSUE=Skin secretion;  
RX MEDLINE=75131227; PubMed=1120493;  
RA Anastasi A., Erspamer V., Endean R.;  
RT "Structure of uperolein, a physalaemin-like endecapeptide occurring  
RT in the skin of Uperoleia rugosa and Uperoleia marmorata.";  
RL Experientia 31:394-395(1975).  
CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,  
CC evoke behavioral responses, are potent vasodilators and  
CC secretagogues, and contract (directly or indirectly) many smooth  
CC muscles.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Skin.  
CC -!- SIMILARITY: Belongs to the tachykinin family.  
DR InterPro; IPR002040; Tachy\_Neurokinin.  
DR InterPro; IPR008215; Tachykinin.  
DR Pfam; PF02202; Tachykinin; 1.  
DR SMART; SM00203; TK; 1.  
DR PROSITE; PS00267; TACHYKININ; 1.  
KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;  
KW Pyrrolidone carboxylic acid.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
FT MOD\_RES 11 11 AMIDATION.  
SQ SEQUENCE 11 AA; 1252 MW; 32867C3E59CDD457 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.4e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1  
|  
Db 6 A 6

# RESULT 53

TKN2\_PSEGU  
ID TKN2\_PSEGU STANDARD; PRT; 11 AA.  
AC P42987;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Kassinin-like peptide K-II (PG-KII).  
OS Pseudophryne guentheri (Guenther's toadlet).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;  
OC Myobatrachinae; Pseudophryne.  
OX NCBI\_TaxID=30349;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Skin secretion;  
RX MEDLINE=90287814; PubMed=2356157;  
RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,  
RA Roberts J.D., Melchiorri P., Erspamer V.;  
RT "Six novel tachykinin- and bombesin-related peptides from the skin of  
RT the Australian frog Pseudophryne guntheri.";  
RL Peptides 11:299-304(1990).  
CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,

CC evoke behavioral responses, are potent vasodilators and  
 CC secretagogues, and contract (directly or indirectly) many smooth  
 CC muscles.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Skin.  
 CC -!- SIMILARITY: Belongs to the tachykinin family.  
 DR PIR; C60409; C60409.  
 DR InterPro; IPR002040; Tachy\_Neurokinin.  
 DR InterPro; IPR008215; Tachykinin.  
 DR Pfam; PF02202; Tachykinin; 1.  
 DR SMART; SM00203; TK; 1.  
 DR PROSITE; PS00267; TACHYKININ; 1.  
 KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;  
 KW Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 11 11 AMIDATION.  
 SQ SEQUENCE 11 AA; 1246 MW; 3A247C37C9CB1AB7 CRC64;  
  
 Query Match 9.1%; Score 1; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 9.4e+04;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 Qy 2 E 2  
 |  
 Db 6 E 6

#### RESULT 54

TKN2\_UPERU  
 ID TKN2\_UPERU STANDARD; PRT; 11 AA.  
 AC P08616;  
 DT 01-AUG-1988 (Rel. 08, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Rugosauperolein II ([Lys5,Thr6]physalaemin).  
 OS Uperoleia rugosa (Wrinkled toadlet).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;  
 OC Myobatrachinae; Uperoleia.  
 OX NCBI\_TaxID=8368;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Skin secretion;  
 RX MEDLINE=80223080; PubMed=7389029;  
 RA Nakajima T., Yasuhara T., Erspamer V., Erspamer G.F., Negri L.;  
 RT "Physalaemin- and bombesin-like peptides in the skin of the  
 RT Australian leptodactylid frog Uperoleia rugosa."  
 RL Chem. Pharm. Bull. 28:689-695(1980).  
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,  
 CC evoke behavioral responses, are potent vasodilators and  
 CC secretagogues, and contract (directly or indirectly) many smooth  
 CC muscles.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Skin.  
 CC -!- SIMILARITY: Belongs to the tachykinin family.  
 DR InterPro; IPR002040; Tachy\_Neurokinin.  
 DR Pfam; PF02202; Tachykinin; 1.

DR PROSITE; PS00267; TACHYKININ; 1.  
 KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;  
 KW Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 11 11 AMIDATION.  
 SQ SEQUENCE 11 AA; 1270 MW; 3293693E59D1A327 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 9.4e+04;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1  
 |  
 Db 2 A 2

RESULT 55  
 TKN3\_PSEGU  
 ID TKN3\_PSEGU STANDARD; PRT; 11 AA.  
 AC P42988;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Kassinin-like peptide K-III (PG-KIII).  
 OS Pseudophryne guentheri (Guenther's toadlet).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;  
 OC Myobatrachinae; Pseudophryne.  
 OX NCBI\_TaxID=30349;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Skin secretion;  
 RX MEDLINE=90287814; PubMed=2356157;  
 RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,  
 RA Roberts J.D., Melchiorri P., Erspamer V.;  
 RT "Six novel tachykinin- and bombesin-related peptides from the skin of  
 RT the Australian frog Pseudophryne guntheri.";  
 RL Peptides 11:299-304(1990).  
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,  
 CC evoke behavioral responses, are potent vasodilators and  
 CC secretagogues, and contract (directly or indirectly) many smooth  
 CC muscles.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Skin.  
 CC -!- SIMILARITY: Belongs to the tachykinin family.  
 DR PIR; D60409; D60409.  
 DR InterPro; IPR002040; Tachy\_Neurokinin.  
 DR InterPro; IPR008215; Tachykinin.  
 DR Pfam; PF02202; Tachykinin; 1.  
 DR SMART; SM00203; TK; 1.  
 DR PROSITE; PS00267; TACHYKININ; 1.  
 KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;  
 KW Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 11 11 AMIDATION.  
 SQ SEQUENCE 11 AA; 1268 MW; 3DBA7C37C9CB1457 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.4e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 E 2  
|  
Db 6 E 6

RESULT 56

TKN4\_PSEGU

ID TKN4\_PSEGU STANDARD; PRT; 11 AA.

AC P42989;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Substance P-like peptide I (PG-SPI).

OS Pseudophryne guentheri (Guenther's toadlet).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Neobatrachia; Hyla; Myobatrachidae;

OC Myobatrachinae; Pseudophryne.

OX NCBI\_TaxID=30349;

RN [1]

RP SEQUENCE.

RC TISSUE=Skin secretion;

RX MEDLINE=90287814; PubMed=2356157;

RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,

RA Roberts J.D., Melchiorri P., Erspamer V.;

RT "Six novel tachykinin- and bombesin-related peptides from the skin of  
RT the Australian frog Pseudophryne guentheri.";

RL Peptides 11:299-304(1990).

CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,  
CC evoke behavioral responses, are potent vasodilators and  
CC secretagogues, and contract (directly or indirectly) many smooth  
CC muscles.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- TISSUE SPECIFICITY: Skin.

CC -!- SIMILARITY: Belongs to the tachykinin family.

DR PIR; E60409; E60409.

DR InterPro; IPR002040; Tachy\_Neurokinin.

DR InterPro; IPR008215; Tachykinin.

DR Pfam; PF02202; Tachykinin; 1.

DR SMART; SM00203; TK; 1.

DR PROSITE; PS00267; TACHYKININ; 1.

KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;

KW Pyrrolidone carboxylic acid.

FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.

FT MOD\_RES 11 11 AMIDATION.

SQ SEQUENCE 11 AA; 1294 MW; 3A247C2CC9CB1AB7 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.4e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 E 2  
|  
Db 6 E 6

# RESULT 57

TKN5\_PSEGU

ID TKN5\_PSEGU STANDARD; PRT; 11 AA.  
AC P42990;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Substance P-like peptide II (PG-SPII).  
OS Pseudophryne guentheri (Guenther's toadlet).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;  
OC Myobatrachinae; Pseudophryne.  
OX NCBI\_TaxID=30349;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Skin secretion;  
RX MEDLINE=90287814; PubMed=2356157;  
RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,  
RA Roberts J.D., Melchiorri P., Erspamer V.;  
RT "Six novel tachykinin- and bombesin-related peptides from the skin of  
RT the Australian frog Pseudophryne guentheri.";  
RL Peptides 11:299-304(1990).  
CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,  
CC evoke behavioral responses, are potent vasodilators and  
CC secretagogues, and contract (directly or indirectly) many smooth  
CC muscles.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Skin.  
CC -!- SIMILARITY: Belongs to the tachykinin family.  
DR PIR; F60409; F60409.  
DR InterPro; IPR002040; Tachy\_Neurokinin.  
DR InterPro; IPR008215; Tachykinin.  
DR Pfam; PF02202; Tachykinin; 1.  
DR SMART; SM00203; TK; 1.  
DR PROSITE; PS00267; TACHYKININ; 1.  
KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;  
KW Pyrrolidone carboxylic acid.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
FT MOD\_RES 11 11 AMIDATION.  
SQ SEQUENCE 11 AA; 1293 MW; 3A247C2CC9CB1457 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.4e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 E 2  
|  
Db 6 E 6

# RESULT 58

TKNA\_CHICK

ID TKNA\_CHICK STANDARD; PRT; 11 AA.  
AC P19850;  
DT 01-FEB-1991 (Rel. 17, Created)

DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Substance P.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Intestine;  
 RX MEDLINE=88204263; PubMed=2452461;  
 RA Conlon J.M., Katsoulis S., Schmidt W.E., Thim L.;  
 RT "[Arg3]substance P and neurokinin A from chicken small intestine."  
 RL Regul. Pept. 20:171-180(1988).  
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,  
 CC evoke behavioral responses, are potent vasodilators and  
 CC secretagogues, and contract (directly or indirectly) many smooth  
 CC muscles.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: Belongs to the tachykinin family.  
 DR PIR; JN0023; JN0023.  
 DR InterPro; IPR002040; Tachy\_Neurokinin.  
 DR Pfam; PF02202; Tachykinin; 1.  
 DR PROSITE; PS00267; TACHYKININ; 1.  
 KW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.  
 FT MOD\_RES 11 11 AMIDATION.  
 SQ SEQUENCE 11 AA; 1377 MW; 21487FE3C9D6C6C7 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 9.4e+04;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 G 3  
 |  
 Db 9 G 9

#### RESULT 59

TKNA\_GADMO  
 ID TKNA\_GADMO STANDARD; PRT; 11 AA.  
 AC P28498;  
 DT 01-DEC-1992 (Rel. 24, Created)  
 DT 01-DEC-1992 (Rel. 24, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Substance P.  
 OS Gadus morhua (Atlantic cod).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Paracanthopterygii; Gadiformes; Gadidae; Gadus.  
 OX NCBI\_TaxID=8049;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Brain;  
 RX MEDLINE=92298992; PubMed=1376687;  
 RA Jensen J., Conlon J.M.;  
 RT "Substance-P-related and neurokinin-A-related peptides from the brain

RT of the cod and trout.";  
 RL Eur. J. Biochem. 206:659-664(1992).  
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,  
 CC evoke behavioral responses, are potent vasodilators and  
 CC secretagogues, and contract (directly or indirectly) many smooth  
 CC muscles.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: Belongs to the tachykinin family.  
 DR PIR; S23306; S23306.  
 DR InterPro; IPR002040; Tachy\_Neurokinin.  
 DR InterPro; IPR008215; Tachykinin.  
 DR Pfam; PF02202; Tachykinin; 1.  
 DR SMART; SM00203; TK; 1.  
 DR PROSITE; PS00267; TACHYKININ; 1.  
 KW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.  
 FT MOD\_RES 11 11 AMIDATION (BY SIMILARITY).  
 SQ SEQUENCE 11 AA; 1315 MW; 214860D759D6C6C7 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 9.4e+04;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 K 5  
 |  
 Db 1 K 1

# RESULT 60

## TKNA\_HORSE

ID TKNA\_HORSE STANDARD; PRT; 11 AA.  
 AC P01290;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Substance P.  
 GN TAC1 OR NKNA OR TAC2 OR NKA.  
 OS Equus caballus (Horse), and  
 OS Cavia porcellus (Guinea pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.  
 OX NCBI\_TaxID=9796, 10141;  
 RN [1]  
 RP SEQUENCE.  
 RC SPECIES=Horse;  
 RA Studer R.O., Trzeciak A., Lergier W.;  
 RT "Isolation and amino-acid sequence of substance P from horse  
 RT intestine.";  
 RL Helv. Chim. Acta 56:860-866(1973).  
 RN [2]  
 RP SEQUENCE.  
 RC SPECIES=C.porcellus;  
 RX MEDLINE=90044685; PubMed=2478925;  
 RA Murphy R.;  
 RT "Primary amino acid sequence of guinea-pig substance P.";  
 RL Neuropeptides 14:105-110(1989).  
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,  
 CC evoke behavioral responses, are potent vasodilators and



CC secretagogues, and contract (directly or indirectly) many smooth  
 CC muscles.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: Belongs to the tachykinin family.  
 DR PIR; A01558; SPHO.  
 DR PIR; A60654; A60654.  
 DR InterPro; IPR002040; Tachy\_Neurokinin.  
 DR InterPro; IPR008215; Tachykinin.  
 DR Pfam; PF02202; Tachykinin; 1.  
 DR SMART; SM00203; TK; 1.  
 DR PROSITE; PS00267; TACHYKININ; 1.  
 KW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.  
 FT MOD\_RES 11 11 AMIDATION.  
 SQ SEQUENCE 11 AA; 1349 MW; 3E757FE3C9D6C6C7 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 9.4e+04;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 R 10  
 |  
 Db 1 R 1

#### RESULT 61

TKNA\_ONCMY  
 ID TKNA\_ONCMY STANDARD; PRT; 11 AA.  
 AC P28499;  
 DT 01-DEC-1992 (Rel. 24, Created)  
 DT 01-DEC-1992 (Rel. 24, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Substance P.  
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.  
 OX NCBI\_TaxID=8022;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Brain;  
 RX MEDLINE=92298992; PubMed=1376687;  
 RA Jensen J., Conlon J.M.;  
 RT "Substance-P-related and neurokinin-A-related peptides from the brain  
 RT of the cod and trout."  
 RL Eur. J. Biochem. 206:659-664(1992).  
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,  
 CC evoke behavioral responses, are potent vasodilators and  
 CC secretagogues, and contract (directly or indirectly) many smooth  
 CC muscles.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: Belongs to the tachykinin family.  
 DR PIR; S23308; S23308.  
 DR InterPro; IPR002040; Tachy\_Neurokinin.  
 DR InterPro; IPR008215; Tachykinin.  
 DR Pfam; PF02202; Tachykinin; 1.  
 DR SMART; SM00203; TK; 1.  
 DR PROSITE; PS00267; TACHYKININ; 1.

KW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.  
FT MOD RES 11 11 AMIDATION (BY SIMILARITY).  
SQ SEQUENCE 11 AA; 1358 MW; 214860DEC9D6D1F7 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.4e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 K 5  
|  
Db 1 K 1

RESULT 62

TKNA\_RANCA

ID TKNA\_RANCA STANDARD; PRT; 11 AA.  
AC P22688;  
DT 01-AUG-1991 (Rel. 19, Created)  
DT 01-AUG-1991 (Rel. 19, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Ranatachykinin A (RTK A).  
OS Rana catesbeiana (Bull frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.  
OX NCBI\_TaxID=8400;  
RN [1]  
RP SEQUENCE, AND SYNTHESIS.  
RC TISSUE=Brain, and Intestine;  
RX MEDLINE=91254337; PubMed=2043143;  
RA Kozawa H., Hino J., Minamino N., Kangawa K., Matsuo H.;  
RT "Isolation of four novel tachykinins from frog (Rana catesbeiana)  
RT brain and intestine.";  
RL Biochem. Biophys. Res. Commun. 177:588-595(1991).  
RN [2]  
RP SEQUENCE.  
RC TISSUE=Intestine;  
RX MEDLINE=94023216; PubMed=8210506;  
RA Kangawa K., Kozawa H., Hino J., Minamino N., Matsuo H.;  
RT "Four novel tachykinins in frog (Rana catesbeiana) brain and  
RT intestine.";  
RL Regul. Pept. 46:81-88(1993).  
CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,  
CC evoke behavioral responses, are potent vasodilators and  
CC secretagogues, and contract (directly or indirectly) many smooth  
CC muscles.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: Belongs to the tachykinin family.  
DR PIR; A61033; A61033.  
DR InterPro; IPR002040; Tachy\_Neurokinin.  
DR InterPro; IPR008215; Tachykinin.  
DR Pfam; PF02202; Tachykinin; 1.  
DR SMART; SM00203; TK; 1.  
DR PROSITE; PS00267; TACHYKININ; 1.  
KW Tachykinin; Neuropeptide; Amidation.  
FT MOD RES 11 11 AMIDATION.  
SQ SEQUENCE 11 AA; 1311 MW; 200D60CC59D40AB7 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.4e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 K 5  
|  
Db 1 K 1

RESULT 63

TKNA\_RANRI

ID TKNA\_RANRI STANDARD; PRT; 11 AA.  
AC P29207;  
DT 01-DEC-1992 (Rel. 24, Created)  
DT 01-DEC-1992 (Rel. 24, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Ranakinin (Substance-P-related peptide).  
OS Rana ridibunda (Laughing frog) (Marsh frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.  
OX NCBI\_TaxID=8406;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Brain;  
RX MEDLINE=92044543; PubMed=1658233;  
RA O'Harte F., Burcher E., Lovas S., Smith D.D., Vaudry H., Conlon J.M.;  
RT "Ranakinin: a novel NK1 tachykinin receptor agonist isolated with  
RT neurokinin B from the brain of the frog Rana ridibunda.";  
RL J. Neurochem. 57:2086-2091(1991).  
CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,  
CC evoke behavioral responses, are potent vasodilators and  
CC secretagogues, and contract (directly or indirectly) many smooth  
CC muscles.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: Belongs to the tachykinin family.  
DR InterPro; IPR002040; Tachy\_Neurokinin.  
DR InterPro; IPR008215; Tachykinin.  
DR Pfam; PF02202; Tachykinin; 1.  
DR SMART; SM00203; TK; 1.  
DR PROSITE; PS00267; TACHYKININ; 1.  
KW Tachykinin; Neuropeptide; Amidation.  
FT MOD\_RES 11 11 AMIDATION.  
SQ SEQUENCE 11 AA; 1352 MW; 3A2460CC59D40B07 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.4e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 K 5  
|  
Db 1 K 1

RESULT 64

TKNA\_SCYCA

ID TKNA\_SCYCA STANDARD; PRT; 11 AA.  
AC P41333;

DT 01-FEB-1995 (Rel. 31, Created)  
 DT 01-FEB-1995 (Rel. 31, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Substance P.  
 OS *Scyliorhinus canicula* (Spotted dogfish) (Spotted catshark).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;  
 OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;  
 OC Scyliorhinidae; *Scyliorhinus*.  
 OX NCBI\_TaxID=7830;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Brain;  
 RX MEDLINE=93292508; PubMed=7685693;  
 RA Waugh D., Wang Y., Hazon N., Balment R.J., Conlon J.M.;  
 RT "Primary structures and biological activities of substance-P-related  
 RT peptides from the brain of the dogfish, *Scyliorhinus canicula*.";  
 RL Eur. J. Biochem. 214:469-474(1993).  
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,  
 CC evoke behavioral responses, are potent vasodilators and  
 CC secretagogues, and contract (directly or indirectly) many smooth  
 CC muscles.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: Belongs to the tachykinin family.  
 DR PIR; S33300; S33300.  
 DR InterPro; IPR002040; Tachy\_Neurokinin.  
 DR PROSITE; PS00267; TACHYKININ; 1.  
 KW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.  
 FT MOD\_RES 11 11 AMIDATION.  
 SQ SEQUENCE 11 AA; 1278 MW; 214860DEC9D6D867 CRC64;  
  
 Query Match 9.1%; Score 1; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 9.4e+04;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 Qy 5 K 5  
 |  
 Db 1 K 1

# RESULT 65

TKND\_RANCA  
 ID TKND\_RANCA STANDARD; PRT; 11 AA.  
 AC P22691;  
 DT 01-AUG-1991 (Rel. 19, Created)  
 DT 01-AUG-1991 (Rel. 19, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Ranatachykinin D (RTK D).  
 OS *Rana catesbeiana* (Bull frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; *Rana*.  
 OX NCBI\_TaxID=8400;  
 RN [1]  
 RP SEQUENCE, AND SYNTHESIS.  
 RC TISSUE=Intestine;  
 RX MEDLINE=91254337; PubMed=2043143;  
 RA Kozawa H., Hino J., Minamino N., Kangawa K., Matsuo H.;  
 RT "Isolation of four novel tachykinins from frog (*Rana catesbeiana*)

RT brain and intestine.";  
 RL Biochem. Biophys. Res. Commun. 177:588-595(1991).  
 RN [2]  
 RP SEQUENCE.  
 RC TISSUE=Intestine;  
 RX MEDLINE=94023216; PubMed=8210506;  
 RA Kangawa K., Kozawa H., Hino J., Minamino N., Matsuo H.;  
 RT "Four novel tachykinins in frog (*Rana catesbeiana*) brain and  
 RT intestine.";  
 RL Regul. Pept. 46:81-88(1993).  
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,  
 CC evoke behavioral responses, are potent vasodilators and  
 CC secretagogues, and contract (directly or indirectly) many smooth  
 CC muscles.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: Belongs to the tachykinin family.  
 DR PIR; D61033; D61033.  
 DR InterPro; IPR002040; Tachy\_Neurokinin.  
 DR PROSITE; PS00267; TACHYKININ; FALSE\_NEG.  
 KW Tachykinin; Neuropeptide; Amidation.  
 FT MOD\_RES 11 11 AMIDATION.  
 SQ SEQUENCE 11 AA; 1350 MW; 3A34256C59D40B07 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 9.4e+04;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 K 5  
 |  
 Db 1 K 1

# RESULT 66

## TKN\_ELEMO

ID TKN\_ELEMO STANDARD; PRT; 11 AA.  
 AC P01293;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Eledoisin.  
 OS Eledone moschata (Musky octopus) (*Ozaena moschata*), and  
 OS Eledone cirrhosa (Curled octopus) (*Ozaena cirrosa*).  
 OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;  
 OC Octopodiformes; Octopoda; Incirrata; Octopodidae; Eledone.  
 OX NCBI\_TaxID=6641, 102876;  
 RN [1]  
 RP SEQUENCE.  
 RA Anastasi A., Erspamer V.;  
 RT "The isolation and amino acid sequence of eledoisin, the active  
 RT endecapeptide of the posterior salivary glands of Eledone.";  
 RL Arch. Biochem. Biophys. 101:56-65(1963).  
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,  
 CC evoke behavioral responses, are potent vasodilators and  
 CC secretagogues, and contract (directly or indirectly) many smooth  
 CC muscles.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Skin.

CC -!- SIMILARITY: Belongs to the tachykinin family.  
 DR PIR; A01561; EOOC.  
 DR PIR; B01561; EOCC.  
 DR PDB; 1MXQ; 18-FEB-03.  
 DR InterPro; IPR002040; Tachy\_Neurokinin.  
 DR PROSITE; PS00267; TACHYKININ; 1.  
 KW Tachykinin; Neuropeptide; Amidation; Pyrrolidone carboxylic acid;  
 KW 3D-structure.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 11 11 AMIDATION.  
 SQ SEQUENCE 11 AA; 1206 MW; 570D7C2559CDDAA3 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 9.4e+04;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 K 5  
 |  
 Db 4 K 4

# RESULT 67

## TKN\_PHYFU

ID TKN\_PHYFU STANDARD; PRT; 11 AA.  
 AC P08615;  
 DT 01-AUG-1988 (Rel. 08, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Physalaemin.  
 OS Physalaemus fuscumaculatus (Neotropical frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Leptodactylidae;  
 OC Leptodactylinae; Physalaemus.  
 OX NCBI\_TaxID=8378;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Skin secretion;  
 RX MEDLINE=66076612; PubMed=5857249;  
 RA Erspamer V., Anastasi A., Bertaccini G., Cei J.M.;  
 RT "Structure and pharmacological actions of physalaemin, the main  
 RT active polypeptide of the skin of Physalaemus fuscumaculatus.";  
 RL Experientia 20:489-490(1964).  
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,  
 CC evoke behavioral responses, are potent vasodilators and  
 CC secretagogues, and contract (directly or indirectly) many smooth  
 CC muscles.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Skin.  
 CC -!- SIMILARITY: Belongs to the tachykinin family.  
 DR PIR; S07201; S07201.  
 DR InterPro; IPR002040; Tachy\_Neurokinin.  
 DR Pfam; PF02202; Tachykinin; 1.  
 DR PROSITE; PS00267; TACHYKININ; 1.  
 KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;  
 KW Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 11 11 AMIDATION.

SQ SEQUENCE 11 AA; 1283 MW; 3293693E59C33457 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.4e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1  
|  
Db 2 A 2

RESULT 68

UF05\_MOUSE

ID UF05\_MOUSE STANDARD; PRT; 11 AA.  
AC P38643;  
DT 01-OCT-1994 (Rel. 30, Created)  
DT 01-OCT-1994 (Rel. 30, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Unknown protein from 2D-page of fibroblasts (P48) (Fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Fibroblast;  
RX MEDLINE=95009907; PubMed=7523108;  
RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;  
RT "Separation and sequencing of familiar and novel murine proteins  
RT using preparative two-dimensional gel electrophoresis.";  
RL Electrophoresis 15:735-745(1994).  
CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown  
CC protein is: 5.5, its MW is: 48 kDa.  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1328 MW; E54835E5CAAABAFA CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.4e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 K 5  
|  
Db 1 K 1

RESULT 69

ULAG\_HUMAN

ID ULAG\_HUMAN STANDARD; PRT; 11 AA.  
AC P31933;  
DT 01-JUL-1993 (Rel. 26, Created)  
DT 01-JUL-1993 (Rel. 26, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Unknown protein from 2D-page of liver tissue (Spot 118) (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;

RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Liver;  
 RX MEDLINE=94147969; PubMed=8313870;  
 RA Hughes G.J., Frutiger S., Paquet N., Pasquali C., Sanchez J.-C.,  
 RA Tissot J.-D., Bairoch A., Appel R.D., Hochstrasser D.F.;  
 RT "Human liver protein map: update 1993.";  
 RL Electrophoresis 14:1216-1222(1993).  
 CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown  
 CC protein is: 5.5, its MW is: 34 kDa.  
 DR SWISS-2DPAGE; P31933; HUMAN.  
 DR Siena-2DPAGE; P31933; -.  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1219 MW; EDABD37F272DDB0A CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 9.4e+04;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 E 2  
 |  
 Db 5 E 5

# RESULT 70

## UXB2\_YEAST

ID UXB2\_YEAST STANDARD; PRT; 11 AA.  
 AC P99013;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Unknown protein from 2D-page (Spot 2D-000K2F) (Fragment).  
 OS Saccharomyces cerevisiae (Baker's yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.  
 OX NCBI\_TaxID=4932;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=X2180-1A;  
 RA Sanchez J.-C., Golaz O., Schaller D., Morch F., Frutiger S.,  
 RA Hughes G.J., Appel R.D., Deshusses J., Hochstrasser D.F.;  
 RL Submitted (AUG-1995) to Swiss-Prot.  
 CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown  
 CC protein is: 6.20, its MW is: 9.2 kDa.  
 DR SWISS-2DPAGE; P99013; YEAST.  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1328 MW; EC38021C0DCB42DA CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 9.4e+04;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1  
 |  
 Db 7 A 7



Search completed: April 8, 2004, 15:47:23  
Job time : 6.15385 secs